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(54) Title: REAGENTS AND METHODS FOR DETECTING GENES RELATED TO MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH AS CHICKEN

(54) Titre: REACTIFS ET METHODES POUR LA DETECTION DE GENES LIES AU COMPLEXE MAJEUR D'HISTOCOMPATIBILITE D'OISEAUX D'ELEVAGE, TELS QUE LE POULET

(57) Abstract

The invention concerns nucleic acid molecules for detecting the MHC genes involved in phenomena of resistance or proneness to the development of virus-induced tumours. The primers prepared from said molecules can be used in a method for genotyping domestic fowl, characterised in that it consists in: amplifying a nucleic acid sample derived from the animal under study using one or several pairs of primers capable of being specifically hybridised with the nucleic acid of a pleomorphic region of the Rfp-Y or B systems of the MHC of said fowl; detecting the resulting PCR products.

(57) Abrégé

L'invention vise des molécules d'acides nucléiques permettant de détecter ceux des gènes du CMH impliqués dans les phénomènes de résistance ou de susceptibilité au développement de tumeurs viro-induites. Les amorces élaborées à partir de ces molécules sont utilisables dans une méthode de génotypage d'oiseaux d'élevage et notamment du poulet, caractérisée en ce qu'elle comprend : l'amplification d'un échantillon d'acide nucléique provenant de l'animal à étudier à l'aide d'un ou de plusieurs couples d'amorces capables de s'hybrider spécifiquement avec l'acide nucléique d'une région polymorphe des systèmes Rfp-Y ou B du CMH desdits oiseaux et la détection des produits de PCR obtenus.

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REACTIFS ET METHODES POUR LA DETECTION DE GENES  
LIES AU COMPLEXE MAJEUR D'HISTOCOMPATIBILITE D'OISEAUX  
D'ELEVAGE, TELS QUE LE POULET

5 L'invention a pour objet la détection de gènes  
liés au complexe majeur d'histocompatibilité (CMH)  
d'oiseaux d'élevage, tels que le poulet. A ce titre, elle  
concerne des molécules d'acides nucléiques permettant de  
détecter ceux des gènes du CMH impliqués dans les  
10 phénomènes de résistance ou de susceptibilité au  
développement de tumeurs viro-induites. L'invention  
concerne également les applications de ces molécules  
d'acides nucléiques, notamment pour le développement de  
tests de génotypage chez les oiseaux d'élevage, en  
15 particulier le poulet, et pour la sélection d'animaux  
d'intérêt.

Les maladies virales infectieuses sont  
redoutées des éleveurs en raison de leur caractère  
20 contagieux qui conduit à des pertes importantes  
d'animaux.

La vaccination a constitué une prophylaxie  
efficace jusqu'à l'émergence de souches hypervirulentes,  
25 rendant nécessaire l'identification des haplotypes  
résistants.

Diverses méthodes ont ainsi été proposées pour  
tenter de sélectionner ceux des animaux qui sont capables  
30 de résister à de telles pathologies et ceux qui sont au  
contraire susceptibles d'être affectés.

Les techniques les plus utilisées en routine  
sont basées sur des polymorphismes sérologiques ou de

type RFLP. Toutefois, ces méthodes ne fournissent pas de connaissances précises sur le phénomène de résistance ou de susceptibilité à la maladie, en particulier par manque de caractère discriminant vis-à-vis des gènes des systèmes B ou Rfp-Y du CMH.

Les travaux des inventeurs sur le séquençage de gènes du CMH a montré la complexité génétique de cette région, ce qui les a conduits à prendre en compte un autre type de polymorphisme, à savoir basé sur la séquence de ces gènes et des régions apparentées, telles que celles de leurs promoteurs et des régions microsatellitaires. Les inventeurs ont ainsi mis au point des moyens pour disposer de molécules oligonucléotidiques hautement spécifiques des polymorphismes observés, permettant d'identifier les parties de gènes, et même les sites impliqués dans le contrôle de la résistance ou de la susceptibilité au développement de tumeurs.

Le caractère spécifique de ces molécules, vis-à-vis d'un gène donné de l'un des systèmes du CMH, en fait des outils discriminants particulièrement fiables pour identifier avec précision la capacité de résistance ou de susceptibilité du poulet étudié, ou d'autres oiseaux, à une infection virale, et pour étudier au niveau moléculaire les séquences du CMH impliquées.

L'invention a donc pour but de fournir des molécules d'acides nucléiques permettant de détecter spécifiquement, chez les oiseaux d'élevage et en particulier chez le poulet, les gènes liés au CMH impliqués dans les phénomènes de résistance ou de susceptibilité au développement de tumeurs viro-induites.



Elle vise également à fournir une méthode et un kit de détection de génotypes de mise en oeuvre aisée en routine.

5 Les molécules d'acides nucléiques de l'invention sont caractérisées en ce qu'il s'agit de molécules, isolées de leur environnement naturel, d'acides nucléiques de gènes codant pour des protéines impliquées dans le contrôle de la résistance ou de la  
10 susceptibilité au développement de tumeurs viro-induites chez les oiseaux d'élevage, telles que celles de la maladie de Marek chez le poulet, avec le cas échéant, les régions qui leur sont attachées, telles que celles du promoteur ou microsateLLitaires. Le terme gène tel  
15 qu'utilisé dans la description et les revendications englobe ces régions.

Ces molécules d'acides nucléiques sont plus spécialement caractérisées en ce qu'elles présentent les  
20 séquences d'acides nucléiques de gènes du système B ou du système Rfp-Y du CMH des oiseaux d'élevage, à l'exception des séquences des gènes de classe II B-L, du gène 17.5, du gène 12.3 et du gène B-FIV de classe I, ou sont capables de s'apparier avec l'un des brins d'un gène  
25 capable de coder pour une protéine telle que définie ci-dessus dans des conditions faiblement stringentes.

L'appariement dans des conditions de faible stringence auquel il est fait référence ci-dessus est  
30 réalisé à température ambiante, dans un milieu 0,1 SSC, avec lavage à température ambiante.

Les gènes de classe II B-L sont décrits dans Immunogenetics 31:179-187, 1990 et Eur. J. Immunol, 1993, 23:1139-1145.

5 Le gène 17.5 appartient à la superfamille des gènes codant pour les lectines et le gène 12.3 à la famille des gènes codant pour des protéines liant la guanine (guanine nucleotide-binding protein). Ce gène est décrit dans Immunogenetics 39:221-229, 1994.

10 Le gène 12.3 est décrit dans P.N.A.S. USA, vol. 86, 4594-4598, juin 1989, Genetics.

15 Le gène B-FIV de classe I est décrit dans Immunogenetics 31:405-409, 1990.

L'invention vise notamment les molécules d'acides nucléiques répondant à ceux des enchaînements de l'un des gènes suivants :

20 . enchaînement du système Rfp-Y

B-FV (figure 1), B-F VI (figure 2) ;

. enchaînement du système B,

25 8.4 génomique (figure 3) ; B-F I (figure 4) ; C12.1 (figure 5) ; DM (figure 6) ; TAP1 (du début de l'exon 2 à l'extrémité 3') (figure 7) ; et TAP2G (figure 8), et autres gènes compris dans la figure 10 et suites 1 à 35.

30 L'étude des séquences d'acides nucléiques des molécules définies plus haut a permis de repérer avec précision les blocs de polymorphismes qui doivent être détectés pour établir un génotypage fiable et précis.

En comparant les séquences de ces blocs, provenant de différents gènes d'un même haplotype ou d'un même gène de différents haplotypes, les inventeurs ont pris en considération les enchaînements divergents et élaboré, pour chaque gène, des oligonucléotides complémentaires de ces enchaînements divergents.

On dispose ainsi d'amorces spécifiques et discriminantes vis-à-vis d'un gène donné du système B ou du système Rfp-Y.

L'invention vise tout spécialement les molécules d'oligonucléotides correspondant à ces enchaînements et comprenant une partie de la région polymorphe des systèmes du CMH du poulet ou autres oiseaux d'élevage.

On rappelle que la région polymorphe peut être dans le gène ou dans une région apparentée telle que les régions microsatellitaires ou celle du promoteur.

Selon un mode de réalisation de l'invention, les polymorphismes sont liés à la fonction des systèmes du CMH.

Il s'agit ainsi avantageusement de molécules correspondant à une partie d'un exon. On citera à titre d'exemple des molécules correspondant à l'exon 2 (domaine  $\alpha$  1) des gènes YF du poulet. Un couple d'amorces approprié est constitué par :

Y-F VI  $\alpha$  1 : GGCCCCGGGATGCCGCGGTTC  
Y-F VI  $\alpha$  1, R : ATCCGCTCACCGCCCTGG

Selon un autre mode de réalisation de l'invention, les molécules oligonucléotidiques correspondent à une partie d'une région polymorphe qui n'est pas liée à la fonction des systèmes du CMH. Des régions préférées de ce type sont des microsattellites.

En considérant par exemple, le gène B-FI, des molécules d'oligonucléotides utilisables pour constituer des couples d'amorces correspondent aux enchaînements suivants :

B-FI : 5' CCA GCA GTC ACT GCA CAT AT 3'  
B-FI, R : 5' AGG TGG AGT GCG CAA AGT T 3', et  
12.1 : 5' ACA CGC AGC AGA ACT TGG TAA 3'  
12.1 R : 5' GGA AGG AAG ACC TTG GAA 3'

Avec les molécules oligonucléotidiques définies ci-dessus et celles élaborées à partir de gènes connus, mais selon la démarche de l'invention, on dispose de jeux d'amorces hautement spécifiques, permettant de déterminer avec précision l'haplotype de l'animal à étudier et de détecter s'il est résistant au développement de tumeurs viro-induites, ou au contraire susceptible d'être affecté.

L'invention vise donc également une méthode de génotypage d'oiseaux d'élevage et notamment du poulet.

Cette méthode est caractérisée en ce qu'elle comprend

- l'amplification d'un échantillon d'acide nucléique provenant de l'animal à étudier à l'aide d'un ou de plusieurs couples d'amorces capables de s'hybrider spécifiquement avec l'acide nucléique d'une région polymorphe des systèmes Rfp-Y ou B du CMH desdits oiseaux,

et

- la détection des produits de PCR obtenus.

Une simple comparaison des résultats obtenus avec un référentiel établi au préalable permet de  
5 déterminer rapidement l'haplotype de l'animal.

L'échantillon d'acide nucléique est constitué en particulier par de l'ADN génomique extrait de matériel biologique de l'animal à étudier ou par ce matériel même, en particulier par du sang de l'animal. Il peut s'agir en  
10 variante d'ADNc, d'ARN ou encore de PNA (polypeptides nucleic acids).

Les amorces sont élaborées à partir des molécules oligonucléotidiques définies ci-dessus et,  
15 d'une manière générale, de tout gène (et région apparentée) codant pour une protéine impliquée dans le contrôle de la résistance ou de la susceptibilité aux tumeurs viro-induites chez les oiseaux d'élevage et notamment de poulet, en particulier les gènes B-L de  
20 classe II, 17.5, 12.3 et B-FIV de classe I.

Il s'agit par exemple d'amorces de régions microsatellitaires permettant de détecter des haplotypes du complexe B, telles que celles élaborées à partir du gène B-FI, et évoquées ci-dessus, ou d'amorces permettant  
25 de détecter des haplotypes du système RFP-Y, et élaborées à partir du gène 17.5, comme le couple :

17.52 : CAG GAT CTG CAC TGG CCA ATA

30 17.5, R1 : GAA TGG CGG TGC TTC CGT GCC TGG

La détection des produits de PCR est effectuée selon les techniques classiques. Ces techniques

comprennent le séquençage, l'électrophorèse, les hybridations avec analyse SSOP ou SSCP.

5 Cette technique sera avantageusement choisie selon la nature du polymorphisme impliqué. Ainsi, dans le cas de polymorphisme de type microsatellite, on détectera avec avantage les produits de PCR selon leur taille en ayant recours aux techniques d'électrophorèse.

10 Lorsque le polymorphisme ne concerne que quelques nucléotides, voire un seul nucléotide, on aura plus spécialement recours, aux fins de différenciation des haplotypes de produits de PCR, aux techniques d'hybridation (analyse sur membrane à l'aide de sondes  
15 spécifiques des séquences d'haplotypes, SSOP ou Sequence Specific Oligonucleotide Probe), de migration différentielle des échantillons dénaturés (SSCP ou Single Strand Conformational Polymorphism), ou de séquençage. De manière générale, cette dernière technique est préférée  
20 compte tenu de la simplicité de sa réalisation.

L'invention fournit ainsi une technique simple et rapide d'établissement du profil génétique d'un grand nombre d'animaux à étudier, ce qui permet de déterminer  
25 les haplotypes et de sélectionner ceux d'intérêt en vue d'un élevage.

De plus, chaque type de gène pouvant être discriminé en utilisant des amorces présentant la  
30 spécificité requise et son appartenance au système B ou Rfp-Y pouvant être établie, il est possible d'effectuer des études fondamentales plus complètes.

L'invention vise également un coffret ou trousse pour détecter le génotype du poulet ou autre oiseau d'élevage selon la méthode définie ci-dessus.

5 Ces coffrets ou trousse sont caractérisés en ce qu'ils comportent les réactifs nécessaires pour la réalisation d'au moins une PCR et du test de révélation.

10 En particulier, ils comportent les amorces pour la PCR, un témoin positif de la réaction, ainsi qu'une notice d'utilisation.

15 Les amorces se présentent sous forme lyophilisée ou en solution ou, selon le mode de détection, sur un support. Le support peut être, de manière classique, une plaque multipuits ou se présenter sous forme de puces à ADN.

20 L'invention vise en outre un système expérimental qui permet d'étudier la résistance au développement tumoral chez le poulet.

25 Il s'agit de lignées d'animaux qui ont été triées génétiquement sur leurs caractéristiques du CMH. En fonction de ces caractéristiques, les lignées sont soit résistantes, soit sensibles vis-à-vis des tumeurs induites par des virus, comme le virus de la maladie de Marek. Cette sélection génétique, qui s'est dans un premier temps effectuée sur des critères sérologiques, a  
30 été ensuite poursuivie sur la base de l'étude du polymorphisme des gènes du CMH. Il s'agit d'un matériel génétique qui est parfaitement défini d'un point moléculaire, et constitue un outil précieux pour l'étude du polymorphisme des séquences de type microsatellite. Ce

matériel, ainsi que le produit du croisement entre certaines des lignées entre elles, a été utilisé pour déterminer les séquences microsatellites du CMH qui sont polymorphes et pour évaluer si ce polymorphisme peut être  
5 corrélé avec les données de typage déjà disponibles pour ces lignées.

D'autres caractéristiques et avantages de l'invention sont exposés dans les exemples qui suivent, dans lesquels il est fait référence à la figure 9  
10 représentant une photo d'électrophorèse de produits de PCR illustrant le test de génotypage de l'invention. On rappelle que les figures 1 à 8, déjà évoquées ci-dessus, illustrent les séquences de gènes selon l'invention.

15

Exemple :

Etude d'haplotypes Rfp-Y du poulet à l'aide d'amorces microsatellitaires.

20

- amplification avec le Kit Expand™ High Fidelity PCR System

. Avec les amorces 17.5 R1/17.52

25

ADN génomique : 1 µg

Oligos prendre : 0,3 µM

dNTP : 8 µl

qsp H<sub>2</sub>O 50 µl

30

On ajoute 50 µl de Mix 2 en mélangeant.

Mix 2 : 0,75 µl d'enzyme

10 µl TP10X avec MgCl<sub>2</sub>

qsp H<sub>2</sub>O 50 µl



Programme d'amplification :

## 30 Cycles

5

94°C	94°C	65°C	72°C	4°C
2'	30''	1'	1'	∞

. Avec B-FI/B-FI, R :

10

ADN génomique : 1 µg

Oligos prendre : 0,3 µM

dNTP : 8 µl

qsp H<sub>2</sub>O 50 µl

15

et ajouter 50 µl de Mix 2 en mélangeant.

Programme d'amplification :

## 30 Cycles

20

94°C	94°C	60°C	72°C	4°C
2'	30''	1'	1'	∞

25 - révélation par électrophorèse sur gel  
d'agarose ou par séquençage.

30 Le test a été appliqué à 9 haplotypes de  
poulet, sélectionnés sérologiquement pour le complexe B.  
Il s'agit des haplotypes B4, B5, B7, B12, B13, B14, B15,  
B21 et d'un haplotype inconnu BX.

Plusieurs individus d'un même type ont été  
étudiés pour B12 (6 individus), B13 (3 individus), B14 (4

individus), B21 (4 individus) et un seul individu pour les autres haplotypes.

5 La figure 9 donne une photo d'électrophorèse sur gel d'agarose à 1 % des produits de PCR obtenus à l'issue de l'étape d'amplification.

10 Les pistes 1 et 27 correspondent aux marqueurs de taille et les pistes (2 à 25) aux produits de PCR des haplotypes suivants : piste 2 : B4 ; piste 4 : B5 ; piste 5 : B7 ; pistes 6 à 11 : B12 ; pistes 12, 13, 14 : B13 ; pistes 15, 16, 17, 18 : B14 ; piste 19 : B15 ; pistes 20, 21, 23, 24 : B21 ; piste 25 : BX (absence de détection pour les pistes 3 et 22).

15 L'examen de cette figure montre que les individus qui ont l'haplotype B12 donnent une même bande et sont donc bien homogènes. La même observation s'applique aux individus B14. En revanche, avec B21, on constate que les profils sont différents, ce qui démontre  
20 l'inefficacité de l'approche sérologique. Compte-tenu de la position de la bande de BX, on détermine qu'il s'agit d'un haplotype B4.

25 L'application pratique de cette méthode revient à soumettre les individus naturellement résistants au protocole décrit ci-dessus en prenant en compte les deux systèmes Rfp-Y et B du CMH et à ne sélectionner parmi des animaux à tester que ceux dont le profil correspond à celui des animaux résistants.

30 L'invention fournit ainsi les moyens de vérifier l'homogénéité des animaux et d'effectuer des sélections rigoureuses en prenant en compte chaque système du CMH, et dans ces systèmes les gènes recherchés.

## REVENDEICATIONS

1/ Molécules d'acides nucléiques isolées de leur environnement naturel, de gènes codant pour des protéines impliquées dans le contrôle de la résistance ou de la susceptibilité au développement de tumeurs chez le poulet, telles que celles de la maladie de Marek, et de régions apparentées auxdits gènes caractérisées en ce qu'elles présentent les séquences d'acides nucléiques de gènes du système B ou du système Rfp-Y, correspondant au complexe majeur d'histocompatibilité des oiseaux d'élevage à l'exception des séquences des gènes de classe II B-L, du gène 17.5, du gène 12.3 et du gène B-FIV de classe I, ou sont capables de s'apparier avec l'un des brins d'un gène capable de coder pour une protéine telle que définie ci-dessus dans des conditions faiblement stringentes.

2/ Molécules d'acides nucléiques selon la revendication 1, caractérisées en ce qu'elles répondent à l'un des enchaînements suivants :

. enchaînement du système Rfp-Y

B-FV (figure 1), B-FVI (figure 2) ;

. enchaînement du système B,

8.4 génomique (figure 3) ; B-FI (figure 4) ; C121 (figure 5), DM (figure 6), TAP1 (du début de l'exon 2 à l'extrémité 3') (figure 7), et TAP2G (figure 8).

3/ Molécules d'acides nucléiques selon la revendication 1 ou 2, caractérisées en ce qu'elles correspondent à une partie des séquences définies dans les revendications 1 ou 2, cette partie étant spécifique

et discriminante pour un gène donné des systèmes B et Rfp-Y.

4/ Molécules d'acides nucléiques selon la  
5 revendication 3, caractérisées en ce qu'il s'agit de  
molécules d'oligonucléotides correspondant à une partie  
de région polymorphe des systèmes du complexe majeur  
d'histocompatibilité du poulet.

10 5/ Molécules d'acides nucléiques selon la  
revendication 4, caractérisées en ce qu'il s'agit de  
molécules d'oligonucléotides correspondant à une partie  
d'exon.

15 6/ Molécules d'acides nucléiques selon la  
revendication 4, caractérisées en ce qu'il s'agit de  
molécules d'oligonucléotides correspondant à une partie  
de région polymorphe qui n'est pas liée à la fonction des  
systèmes du CMH, telle que les régions  
20 microsatellitaires.

7/ Méthode de génotypage d'oiseaux d'élevage et  
notamment du poulet, caractérisée en ce qu'elle comprend

25 - l'amplification d'un échantillon d'acide  
nucléique provenant de l'animal à étudier à l'aide d'un  
ou de plusieurs couples d'amorces capables de s'hybrider  
spécifiquement avec l'acide nucléique d'une région  
polymorphe des systèmes Rfp-Y ou B du CMH desdits  
30 oiseaux,

et

- la détection des produits de PCR obtenus.

8/ Méthode selon la revendication 7, caractérisée en ce que les amorces sont élaborées à partir des molécules selon l'une quelconque des revendications 3 à 6, et de tout gène (et région apparentée) codant pour une protéine impliquée dans le contrôle de la résistance ou de la susceptibilité aux tumeurs viro-induites chez les oiseaux d'élevage et notamment de poulet, particulièrement les gènes de classe II B-L, 17.5, 12.3 et B-FIV.

10

9/ Méthode selon la revendication 7 ou 8, caractérisée en ce que la détection des produits de PCR est effectuée par séquençage.

15

10/ Coffret ou trousse pour le génotypage d'oiseaux d'élevages et notamment du poulet, caractérisé en ce qu'ils comportent les réactifs nécessaires pour la réalisation d'au moins une PCR et du test de révélation, selon la méthode de la revendication 8 ou 9, en particulier les amorces élaborées à partir des molécules d'acides nucléiques selon l'une quelconque des revendications 3 à 6.

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Figure 1BF V

## B-F V

GGC CCC GGG ATG CCG CGG TTC GTG ATC GTC GGG TAC GTG GAC GAC AAA ATC TTC GGT  
ACC TAC AAC AGT AAG AGC AGG ACT GCA CAG CCT ATC GTG GAG ATG CTG CCG CAG GAG  
GAC CAG GAG CAC TGG GAC ACG CAG ACC CAG AAG GCG CAG GGC GGT GAG CCG GAT TTT  
GAC TGG AAC CTG AAC AGG CTG CCG GAA CGC TAC AAC AAA AGT AAA GGT GAG CGT GGG  
GGA AGC TGC AGC GCG ATG CGT CTG GGA CAG GAG CTC TGT GTG CCG AGG GTG TCC GCC  
AGC CCC ACT GAG GTG TGG CCG TGC CCC ACG CCC AGC TGT GCT GGG CCG TCC ATG TGT  
GGT GGC ACT GTC CCT GGG CCG CCC TGC TCC TGC GCC CAC CCA CCC CAC CCC AGC CTC  
ATG GCA CTC GCG GTG CCC CAC AGC CCT AGA AGC CTC TCA CCT ATT ACT CTG GCT GTG  
CCT CAG GGT CTC ACA CGA TGC AGA TGA TGT TTG GCT GTG ACA TCC TGG AGG ACG GCA  
GCA TCC GAG GGT ACG ATC AGT ATG CAT TTG ATG GGA GGG ACT TCC TTG CCT TTG ATA  
TGG ACA CGA TGA CGT TCA CCG CGG CGG ATC CAG TGG CTG AAA TCA CCA AGA GGA GAT  
GGG AGA CAG AAG GGA CGT ATG CTG AGA GAT GGA AGC ATG AGC TGG GGA CTG TCT GTG  
TTC AGA ACT TGA GGA GAT ACC TGG AGC ATG GGA AGG CAG CGC TGA AAA GGA GAG GTG  
AGG ATG GGA GGG GGA CGT GGG GCT GGG CTG GGT GTG GGG CAG AGG CTC AGT GTG GGG  
TGC TCA GCC CGG CCC ACA ACG TCA CCC ACC TGC AGT GCA GCC CGA GGT GCG AGT GTG  
GGG GAA GGA GGC CGA TGG GAT CCT GAC CTT GTC CTG CCA CGC TCA CCG CTT CTA CCC  
GCG GCC CAT CAC CAT CAG CTG GAT GAA GGA CGG CAT GGT CCG GGA CCA GGA GAC CCG  
CTG GGG GGG CAT CGT GCC CAA CAG CGA TGG CAC CTA CCA CGC CTC GGC TGC CAT TGA  
TGT GCT GCC GGA GGA TGG GGA CAA GTA TTG GTG CCG CGT GGA GCA CGC CAG CCT GCC  
CCA GCC TGG TCT CTT CTC ATG GGG TGA GCT GGC AGC GTG GGG CAC GTG GGG TTG GGA  
TTC GCA GGC TGC CCC TTC CTT TAC TGA CAA CGG CGC TCT CCT CCA GAG CCG CAG CCC  
AAC CTG ATT CCC ATT GTG GCA GGG GCG GTC GTT GCC ATC GTG GCT GTC ATC GCT GCG  
GTC GTT GGA TT

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Figure 2B-FVI

GGC CCC GGG ATG CCG CGG TTC GTG ATC GTC GGG TAC GTG GAC GAC AAA ATC TTC GGT  
ATC TAC GAC AGT AAG AGC AGG ACT GCA CAG CCC ATC GTG GAG ATG CTG CCG CAG GAG  
GAC CAG GAG CAC TGG GAC GCG CAG ACC CAG AAG GCC CAG GGC GGT GAG CCG GAT TTT  
GAC TGG TTC CTG AGC AGG CTG CCG GAA CGC TAC AAC AAA AGT GGA GGT GAG TGT GGG  
GGA AGC TGC AGC GCG ATG CGT CTG GGA CAG GAG CTC TGT GTG CCG AGG GTG TCC GCC  
AGC CCC ACT GAG GTG TGG CCA TGC CCC ACG CCC AGC TGT GCT GGG CCG TCC ATG TGT  
GGT GGC ACT GTC TCT GGG CTG CCC TGC TCC TGC GCC CAC CCA CCC CAC CCC AGC CTC  
ATG GCA CTC GCG GTG CCC CAC AGC CCA AGA AGC CTC TCA CCT ATC ACT CTG ACT GTG  
CCT CAG GGT CTC ACA CGA TGC AGA TGA TGA TCG GCT GTG ACA TCC TGG AGG ACG GCA  
GCA TCC GAG GGT ACG ATC AGT ATG CAT TTG ATG GGA GGG ACT TCC TTG CCT TTG ATA  
TGG ACA CGA TGA CGT TCA CCG CGG CGG ATC CAG TGG CAG AAA TCA CCA AGA GGA GAT  
GGG AGA CAG AAG GGA CGT ATG CTG AGA GAT GGA AGC ATG AGC TGG GGA CTG TCT GCG  
TTC AGA ACT TGA GGA GAT ACC TGG AGC ATG GGA AGG CCG CAG TGA AAA GGA GAG GTG  
AGA ATG GGA GGG AGA CGT GGG GCT GGG CTG GGT GTG GGG CAG GGG CTC AGT GTG GGG  
TGC TCA GCC CGG CCC ACA ACA TCA ACC ACC TGC AGT GCA GCC CGA GGT GCG AGT GTG  
GGG GAA GGA GGC CGA TGG GAT CCT GAC CTT GTC CTG CCA CGC TCA CCG CTT CTA CCC  
GCG GCG CAT CGC CAT CAG CTG GAT GAA GGA CAG CAT GGT CCA GGA CCA GGA GAC CCG  
CTG GGG GGG CAT CGT GCC CAA TAG GGA TGG CAC TTA CCA CAC TTC GGC TGC CAT TGA  
TGT GCT GCC GGA GGA TAG GGA CAA GTA TCG GTG CCG CGT GGA GCA CGC CAG CCT GCC  
CCA GCC TGG CCT CTT CTC TTG GGG TAA GCC TGG CAG CGT GGG ATG TGT GGA GTT GGG  
ATT TGG GGG CCG CCC CTT TGT TTA CTG ACA ACG GTG CTC TCC CCC AGA GCC GCA GCC  
CAA CCT GAT CCC CAT TGA GGC TTG GCT GGT CGT CCC CTT GGT GGT TCT CTT CGT TGC  
TTT GAT TGC ATT

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8.4 génomiqueFigure 3

GGA TCC GGG GTG GGT GGC AGT GGC TGT GTT TAG GTC GGC CTG TGG GGA AAG  
 CCG GGT TGT CCC ACC CAT GTC CCC TCT TCC AAC ACT GTT CCT GAA TGA GTT  
 TTC CCT CTC CGA CCC TTT TTT TAA TGG GTT TCA GGG ATT TAA AAT TAA TAT  
 TGA CGA AGT GAC GGA GGG GGT GGG GCC ACA GCG GAG CCG AAA GCG AAA GCA  
 GCG GAG AGC AAT GGC TGC GGG GCT GCG GCT GCT GCT GGC GGG TGA GAC CCG  
 ACC CCC CCC GGC CCC CTC ATG TCC CAC CAC CCA TAT CGC CCC CCC CCC TCC  
 TCC TCG CCC CAT GCT GAG CCT CTC CCC CAC CCC CAG GGC TCT GCT GGT CCC  
 AAT TTA GGG TGG AAG ACG CCG CCT CCC CTC CGC CCC CCC CCG CTC CGG TGC  
 GCT GCG CGC TGC TGG AGG GGG TGG GGC GCG GGG GAG GGC TGC CGG GGG GGG  
 GCA ATG CCC GTC CTG CAC TGC TGC GCT TTG GGG GGG ACG CGG AGA CCC CTC  
 CCG AAC CCG GCC CGG AGC CCG AAG TCA CCT TCA ATG TCA GCG GTA CGT GGG  
 GAC CCC CGT CAC TGT GCT GTG CGC CTC CTT TAT CCC CAC CCC CCT CCA TGT  
 CCC CAT CTC CTT TAC TTC CCA CAA TGC TCC CAT CCC CCC CAG AAT GTC CCC  
 AGA GTC CCC CAA ACC CCC ATG ACC CCC CCC ACG ACC CCT GGT TCC CAT TAC  
 CCT CTC ACG TCC CCC AGT GTC CCC AAG ATT CCC ATT ACT CCC CGT ATC CCC  
 ATT ATC CCC AAA ATG TCC CCC AAT GTT CCC ATC ACC CCA ATG TTC CCA AGG  
 TCC CTA TCG CTC CTC AAT GTC GCT ATG ATC CCT ATT CCC AAA ATG TCA CCA  
 ATG TCC CCA AAA TCC CCA TTA TCT CCC ACC TCT CCA AAG TCC CCA AGA TCC  
 CCA TTA CCC CCA ATA TCC TCA TTA CAC CCC AAA TGT CCC CAA TGT CCC CTC  
 CAT GTC CCC CAG AGA CCC CAT TAG CCC CAA TAG CTC CCA AAC TGT CCC CAG  
 TGT CCC CAT TAA CCC CAA AAT GAC CCC ATT ACG CCC CAC ACC CCT CCC AAC  
 CCC ATG CCC TCA GAC CCC TTC ATC CCT CTC ACT CCT CTC TCC CTC GCA GAC  
 CCC TGG GGG ACT CTA GCC CCA CTC GGG TCC CCC CCC GGA CTC CCC CCA GCT  
 GCG AAC TGA ACC CCA CGA ACC CCC AGA CCG GCT CTG ACC CAT GGA GCC GCC  
 CTC TGC ACC CCG ACG CCC GCA GCC CCC CAA CCG CGG GGG GGC AGT GGT GGG  
 TGG CGG CGG TGG GGA CCC CGC AGT ACG GTG TCA CTG CGC TGC TGC AGG GGG  
 GGA TGG GCA CAG AAG GAA CCA TCA CTG CCG CCG GTA AGG GGG AAC TTG GGG  
 TGT CCC TCC CTG GGT GTC CCC ATG TCC CTA TCT GTC CCC CAG TGT GTC CCC  
 ATT TGT CCC CTC CTC TGC ATG TGT CCC AAT GTC TCC ATA CAT CCC ATA ATA  
 ACC ATA TGT CCC CAC TCA TCC CCA TAT TCC CCA TGT GTC CCC ATA TCC CCA  
 CAC ATC CCA GTG TGC CCC AAC ACA TCC CCA TGT GCC CCC CCC CAT GCA TCA  
 CTA CCA TCC CCC TAT CCC CCA AGT GTC CCT GTG TCC CTG CAG TTT CTC CCT  
 GTC CTC ATG TGT TCC CAT GTC TCC ATG TCA CTG TGT CCC CGT GTC CCC ACA  
 CAT CAC CAT GCC CCC CAC TGC AGC GCC CCC ATG TCC CTT CAC CTC TCC ATG  
 TCC CCC AGT GTC CCC TAT CCC CTC ATT GTC CCC ATG CCC CCT CAC CTC CCC  
 GTG TCC CCC GTG TCC CTA TGT TCC CCT GGT GTT TCC ATG TCC CCT CAT GCC  
 CCC ATG TCC CCT CAT GTC CCC ATA TCC CCC AGT GTC CCC ATG TCC CTT CAC  
 CTC CCC ATG TCC CCC AAT ATT CCC ATA TCC CCT CAC CTG CCC ATT TCC CCC  
 CGA TGT TCC CAT GTC CCC GCA CCT CCC CAT GTC TTC ACA GTG GCC CTG GCG  
 GTG CTC ACC CAC ACC CCG ACC CTC CGG GCC CGT GTG GGG TCC CCC ATC CAC  
 CTG CAC TGC GCC TTC GCT GCC CCC CCA TCC TCC TTT GTC CTC GAG TGG CGT  
 CAC CAG AAC AGG GGT GCG GGG AGG GTC CTG CTG GCC TAT GAC AGT TCC ACC  
 GCC CGC GCC CCC CGC GCC CAC CCC GGG GCC GAA CTG CTG CTG GGG ACA CGG  
 GAT GGG GAC GGG GTG ACA GCG GTG ACA CTG CGG CTG GCG CGG CCA TCA CCG  
 GGG GAT GAG GGC ACC TAC ATC TGC TCC GTG TTC CTG CCC CAC GGG CAC ACA  
 CAG ACA GTG CTG CAG CTC CAC GTC TTT GGT GCG TCC ATG TGG GGC AGG CGG  
 TGT TCC TAT GGG GTG TGG GGT TGG GCA GTG TTC CTA CGG AGT GTG TAT GAC  
 TGG GTG GTA TTC CTA TTG CTC AGA TAG GAC ATA TGG GAG CAG GCG GTA TTC  
 CTA TGG GGC TGT AGG GTG GAT GGG ACT GGG TGA TAT TCC TGT GGG GGC TGT



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AGG GTG GAT GGG ACT GGG TGG TAT TCC TAT GGA GGC TAT AGG GTG GAT GGG  
ACC GGG TGG TAT TCC TAT GAG GAC TAT AGG ATG GGG TGG CAT CAT CCC ATA  
GTT CAC CTG TAG GTT TAT AGG GGG GGA TGA GCC CTA TAC AGC GTA TGG GCT  
ATA TGG ACC GAT GTC CCC CCA CAT GTC TCC AGA GCC CCC CAA GGT GAC GCT  
GTC CCC GAA GAA CCTGGT GGT GGC CCC GGG GAC GTC AGC AGA GCT ACG CTG  
CCA GTC TGG CTT CTA CCC CTT GGA TGT GAC GGT GAC GTG GCA GCG CCG CGC  
CGG GGG CTC GGG GAC ATC ACA GTC ACC CAG GGA CAC AGT GAT GGA CAG CTG  
GAC TTC AGG TCA CCG CCA GGC AGC CGA TGG AAC CTA CAG CCG GAC GGC GGC  
AGC ACG GCT GAT CCC CGC ACG CCC CCA ACA CCA CGG GGA CAT CTA CAG CTG  
CGT TGT CAC CCA CAC TGC ACT GGC CAA ACC AAT GCG TGT CTC CGT CCG ACT  
GCT CCT GGC TGG TGA GGG GGG ATG TGG GGA TAT TGG AAA CAC GTG GAG GTA  
TTG GGA TGC TGG GAC CAT GGT TAG GAG GGT CTG AGG GAC ATC AGG ACC ATG  
GCC TGG GAC AAT GGG AGA TCA TGG ATT TGG GTT GGG GAC CCC ACC CAG GAT  
GGT GAC ACT GTG CTT AGG GCT GTC GTT GTC CCC ACA GGC ACC GAG GGA CCG  
CAC CTG GAG GAC ATC ACG GGG CTC TTC TTG GTG GCC TTT GTC CTC TGT GGC  
CTC ATC CGT TGG CTC TAC CCT AAA GGT GAG TGC TGT TCC CAC ATC CCA GTG  
CCC CCA CAT CCT CAC ACC CCA ATA TCC CAA TGG CCC ATG TCC CCA TGA GCA  
ATG TCA CTA TGT CCC AAT ATC CTA ATG ATG CTG TGT ACC CAT GTG TCC CCA  
TGT CCC TAT TCC ACT CAC TCT TTC TCT CCC CTC AGC TGC ACG ACC CAA AGA  
GGA AAC CAA GGT AAC ATT CCT CCC CAA AAA CCC CAA ATC CCC CAA AAC ACC  
TCC AAG CAC CCC AAA ACT CAC CAT TCT CAT TCC CCC CCC CCC CCC CCC  
CCC CAT GCC TTG CAG AAA TCG CAG TGA CCT CCA CTC CAG CTC TCA GCA CCT  
CAG CTC CAG ATA AAG AGT TTT TCA CCC CAA AGT TAT ATA TGT GTG GTG GTG  
TCC CCA CAG ATC TGG GTG CAG AGG GGG GAG AAA TGG GGG CAA ACT GGG AGC  
AGT GGG AGC AGT GGG AGG AAG TCC TGG GTT GGT GAG GCA GAT GAG TGG CAC  
CTG GGG ACA TCT GGG TGC CAT CCC TTG TGG ACA TCT GGG TGA CAC TGC ATT  
GCC TTG GGT GAC ATT GGG ATC CTC AGG TCA CTG CAG

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Figure 4

B-FI

GT CGA CCGGAT CTGGATAGGT CGT CAGT CAT CCTAATTAAGGAGGGA CAA CAGTGAATGGG  
GAGGAG CCGATGA CT CAGG CTGGGAGTGGT GAT CCCAGAGGTTT CCT CTG CTGT CAGTGAC  
T CCGTG CTTT CGCTTT CGCTT CA CAA CCTGAGGGAG CG CATT CTGCCTGGCG CCCGATGAC  
GT CA CATAAA CCCCCGA CTGCCATTGG CGGAGAGG CGA CGGAGGAG CCAATGGGGG CGCGG  
GG CCGGG CGGAGGAGTAGGAAAAG CTGAAGGA CGTG CG CTGGGTG CGG CGGA CTGAGAGT  
G CAG CCGTGTGAGG CGATGGGG CCGTG CGGGG CG CTGGG CCTGGGG CTG CTG CT CG CGCC  
GTGTG CGGGG CGG CGG CCGGTGAGTG CGG CCGGA CCGGA CCCCT CCCCG CCTGTAA CCCC  
A CCCC GGG CTGTG CCGTGGGAT CCT CAGA CCCCCA CCG CGG CT CAGG CCT CG CTG CCG  
T CCG CCCCCG CAGAG CT CATT CCTG CCGTA CGT CATA CGG CGATGA CCGAT CCGGCC  
CCGGG CTG CCGTGGT CTGTGA CGTGGGGTACGTGGA CCGGGAA CTCTT CGTG CACTACAA  
CAG CA CCG CGCGGAGGTACGTG CCCCCA CCGAGTGGATGGCGG CCAACA CCGA CAG CAG  
TA CTGGGATGGA CAGACG CAGAT CCGA CAGGG CAATGAG CCGAGTGTGGAAGT GAG CT TGA  
A CA CA CTG CAGGAA CGATA CAA CAGA CCGG CCGT GAG CA CGG CCGGG CCG CGG CT CCGT  
GGGTGTGGGATGGG CT CATGG CG CAGTG CCG CCA CA CCCCCAGG CCGTGG CCGTGG CCGG  
G CGG CA CCGT CCGGGG CTG CCGT CA CAG CCCCCA CCG CG CT CCGGGT GCG CGT CCGGG  
GGGA CCCCCA CCGAT CCGG CTG CAGTGGGAG CCGGAG CCGGAGGGG CCCCT CACCCCT  
G CCGG CTGTGTTT CAGGGT CT CAAA CCGTG CAG CTGATGTACGG CTGTGACAT CCT CGAG  
GATGG CACCAT CCGGGGGTAT CAT CAGA CAG CTA CAGTGGGAGAGACTT CATTG CTTT CG  
A CAAAGG CA CGATGACGTT CACTG CGG CAGTT CCAGAGG CAGGTT CCA CCAAGAGGAAAT  
GGGAGGAAGGAGGTGTTG CTGAGAGGTGGAAGAGTTA CCTGGAGGAAA CCGT CCGTGGAGGG  
G CTG CCGAGATA TGTGGAATA CCGGAAGG CTGAG CTGGG CAGGAGAGGTGAG CCGGGT CCG  
GGTGGGGGGGGGGGGGGGG CCGA CG CAGTGTGGGGT CCGA CCGTGGGG CCGGGG CT CAT CCGT  
GGGAG CT CAG CCGGCCCT CACTG CCG CCA CCA CAGAG CCG CCTGAGGTG CAGTGTGG  
GGGAAGGAGG CTGA CCGGAT CCTGACCTTGT CCTG CCG CG CT CAGGCTT CTA CCGG CCGC  
CCAT CG CCGT CAG CTGG CTGAAGGACGG CG CCGTG CCGGG CAGGACG CCCAGT CCGGGGG  
CAT CCGT CCAACGG CGA CCG CACCTA CCA CACCTGGGT CACCAT CGATG CG CAG CCGGGG  
GACGGGGACAAGTA CCACTG CCG CCGTGGAG CACG CAG CCGTGGGG CCGGG CCT CTA CT  
CGTGGGGT GAGT GAGGGGATGTGGGG CTGGGGGG CTG CCGG CTG CCCCTT CCCCTG CTGAT  
GG CCGG CT CT CCCCCAGAG CCG CCA CAG CCAACCTGGTG CCGAT CCGTGG CCGGGGTGGC  
CGT CG CCA TTGTGG CCA CT CG CCA CTGTGGT TGGT TGGATT CAT CAT CTA CAGACG CAC  
G CAGGTAAAAG CAGAGGGTG CAGG CCGG CAGTGGGG CTGTAGGGGGAT CTGGGT CCCCC  
CTTGGGAG CCCCCA CCGTGTGTGATGTGAACCTGTGATGAAGCAT CT CT CTGT CCG CAG  
GGAAGAAGGGGAAGGG CTA CAA CAT CG CG CCGGTGAGT GATGAGGG CAG CG CTGT CCCCC  
ACCT CTG CCCAGTG CCAGGGTGGT CCTGGGGT CCTG CT TT CT CCAAGGTA CCGATT CCT  
GGTG CT TGGGG CTG CT CCA TG CCCCATAGGGAG CACAGGG CTGGAT CT CACAG CTGTT CCT  
CCCTTATAGA CAGGGAAGGTGGAT CCAG CAG CT CGAG CACAGGTG CCGTGTGGGG CTGTGG  
GTTGGGAGGGG CCGTGTG CT CT CTGTGGTA CTGCCAGGG CTGGG CTATG CTGGGG CT CT  
G CCGGGAGAC CCCCCGAG CAGAGGGT TGGGATGTGAA CCTGG CCGGTGGGACAT CAT CCC  
TT CT CAT CCA CAGGGAG CAA CCG CCA CTGAGTG CTGTGCTT CAG CCGT CAGGAG CC  
AA CAGT CCA CACAG CATT TGGGGT CCGTGTGGA CACAG CCGCAT CCT CCGTGA CCT CT CA  
CAT CT CATT CTGCTT CCTATG CTGA CTGTTATG CTTTG CCGTGA CTGCTT CCTGTGAAATA  
AAATGATGGG CATT CTGTG CT CAG CT TG CCTG CATT CTG CACAGTG CTGTGGTTGGGGAT  
GGGGTGGGTGAGAGGA CCGTGT CAGT TGG CTG CT CAGGGTGCAGATGTGG CCGTGTG CT  
GAGTAC CCACTG CCGT CCCCCCTAT CTG CCTG CTG CT CACT CCCCCCT CCGTGA CCCCCAT  
CCCTT CT CACCT CT CCGTGTGAAC CCGATG CTGGTGGT TG CTGTG CT CCGTGT CCGTGG CAG  
AACT CT CATT TT CCAATGG CAT CCGTGGGTGTGGGATGTGGT CT CCGTGGT CCT CCCCC  
CAG CAGT CACTG CACATAT CCCCCCACTT CCCCCCTAGGT TGTGT CCA CAG CACT CCT  
ATTT CCGT CT CCG CCCCCCCCCCCCCCCCCCG CCGCAT CAG CTG CCGT CTG CAAT CCT CAC  
CCTTG CCA CACA CAA CTTTG CG CACT CCACT CCGT CAT CCG CCGCTT CCCCCAG CT CT C  
CTGT CCGTGTGG CCCCCCT CCCCCCCCCCAT TGTACCTA CACCCAAATAAATATGTTT  
GTTCTG CTGCCCT CAG CCGT CT CCGTGGTTATTT CCCCCGATTGTGTGTGGGGG CG

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TCCGCTCTTCACCCTGGGGGGAAGGGGCTCTGGGGGTCCCTCATTCTCCCTGCACTTCTTA  
CAGCACCGGGACTCCCGCGCTGAGATCCCATCACACCCGGGTACAAACATGCGGCTTTATT  
CCCAGTTCGTGTGCCACCCCGGCCCTGGTGGCACTCAGTGGCACCGCAGTCCATGCAGT  
GGCCGTTGTGTGTGTGTACAGCAGCGGTACC

## 12.1

## Figure 5

ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGC  
ACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCCATAGTTGCCTGCAAC  
TCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCC  
AGTGCTGCAATGATACCGCGAAGACCCACGCTCACCGGCTCCAGATTTAT  
CAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCA  
ACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT  
AAGTAGTTCGCCAGTTAATAGTTTTCGCAACGTTGTTGCCATTGCTGCAG  
GCATCGTGGTGTACGCTCGTCTGTTTGGTATGGCTTCATTAGCTCCGGT  
TCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGC  
GGTTAGCTCCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTTGGCCGCGAG  
TGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCTATG  
CCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATT  
CTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAACAC  
GGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGA  
AAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATC  
CAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTA  
CTTTCACCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCA  
AAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCT  
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGAT  
ACATATTTGAATGTATTTAGAAAAATAAAACAAATAGGGGTTCCGCGCACA  
TTTCCCCGAAAAGTGCCACCTGACGCTAAGAAACCATATTATCATGAC  
ATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAAT  
TCCCGCCCGTAGCGCGCGCGCACCCAGCCGGCATCGCACCCGAGCACCAGC  
TCCCGCGTCGTCCAGATGCCACGGGCCACGTCGAGGCCGACGGGGAGAA  
ATACACGTACCTACCTGGGGATCTCAACAGGCCCCGGGTGGCCAACCAGG  
TCGTGGACGCGTTGTGCAGGTGCGTGATGTCCAGCTCCGTCTCGGGTGC  
CGCCGGGCCCCAACCGGCGGTGCGGGGGGGCGGTGTATCACGCGGCCCGCT  
CGGGTGGCTCGCCGTCGCCACGTTGTCTCCCCGCGGGAACGTCAGGGCCT  
CGGGGTGAGGACGGCCGAAAACGTTACCCAGGCCCGGGAACGCAGCAAC  
ACGGAGGCGGCTGGATTGTGCAAGAGACCCTTAAGGGGGGCGACCGAGGG  
GGGAGGCTGGGCGGTGCGCTCGACCGTGGTGGGGGGCGGGCAGGCTCGCGT  
TCGGGGGGCCGGCCGAGCAGGTAGGTCTTCGGGATGTAAAGCAGCTGGCCG  
GGGTCCCGCGGAAACTCGGCCGTGGTGACCAATAACAAAACAAAAGCGCTC  
CTCGTACCAGCGAAGAAGGGGCGAGAGATGCCGTAGTCAGGTTTAGTTCTG  
CCGGCGGCGCCAGAAATCCGCGCGGTGGTTTTTGGGGGTGCGGGGTGTTT  
GGCAGCCACAGACGCCCGGTGTTCTGTCTGCTCAGTCCAGTCGTGGA  
GCCAGGCCATCCAAAAACCATGGGTCTGTCTGCTCAGTCCAGTCGTGGA  
CCTGACCCACGCAACGCCCAAAATAATAACCCCCACGAACCATAAACCA  
TTCCCCATGGGGGACCCCGTCCCTAACCCACGGGGCCCGTGGCTATGGCA  
GGGCTTGCCGCCCCGACGTTGGCTGCGAGCCCTGGGCCTTACCCGAACT  
TGGGGGGGTGGGGTGGGGAAAAGGAAGAAACGCGGGCGTATTGGCCCCAAT  
GGGGTCTCGGTGGGGTATCGACAGAGTGCCAGCCCTGGGACCGAACCCCG  
CGTTTATGAACAAACGACCCAACACCGTGCGTTTTATTCTGTCTTTTTAT  
TGCCGTCATAGCGCGGGTTCCTTCCGGTATTGTCTCCTTCCGTGTTTCAG  
TTAGCCTCCCCCATCTCCCGGGGTGGGCGAAGAACTCCAGCATGAGATCC  
CCGCGCTGGAGGATCATCCAGCCGGCGTCCCGGAAAACGATTCCGAAGCC  
CAACCTTTCATAGAAGGCGGCGGTGGAATCGAAATCTCGTGATGGCAGGT  
TGGGCGTCGCTTGGTCCGTCATTTCAACCCAGAGTCCCGCTCAGAAGA  
ACTCGTCAAGAAGGCGATAGAAGNNN

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TGGGGTCTCTTTGGTCTGATGGAGAGAGGTTGGCACCAAGGTAAGTCGC  
TGCCTACATCACCCTGGTGTCTCTCAGCAGCTGGTGTAAATTTCTG  
CCATCTGGGCTATTTCTGTAGAAAGCAAAGAAGCTCTGCTGGTGGGCAGC  
TCATCTCCCAAGTGTGAAAAAGCAAATGCAACGCATGCACCCTGCTATCC  
ATGTGGBCCYAKCCCTCTCCATCAGCTGTTGAAGGAGAAATCTGCACTCA  
GAAGAGATTGAATTGGGCTCAGATCTGGCTTGGGAAGATGATGATTCCAA  
CCAGAGTCCAGGAGACTTTGGGGAATGCATGAATCCTATAGGAAAATGGA  
TAACCCTTCATCCAAGAGCAAGCTGGCATGATGCTCTGGGGTGAAAACCC  
ATAATGCCACCTGGTTTTAAGGTTTGGGGTGGCTTACAATGTGCAGCTCT  
GCTTCCGGCGAGGCACTGGGAGCCCTAAACCCATGGAGAGGTCAAACCAG  
TGCTGGAGGTCATTGTGGGCCAGCTGCAATGGGAGGTAGGCAATTATGG  
ACATCGCTGAAGCCACCCACGCTCTGGGGAACCTTGGGTTTTACCTTTC  
ACTGCACTTTAATGGGATTTCTCATCAATGTCTGCATGTTCTTGGCCACC  
TGTTTAAAAATATAATAATAATAATTAATCTTTTGCCCCACTGCGGGAT  
GAGCAGCTGGTGGTTCCCAGCTCACAATAAACCACACTTGAGACTCCCTG  
GAGAATTCGCTTTCTTTTGCAGCTGGTTCCATGKGGGSYKTTACGCC  
CTCTGCAGCTCATAGGCTTTTCTTACAGCCTCTGCTCCACCTATTGCTG  
AAAAGGGGGAAATTTGAGATGGATCCATTTTGTGAACATCTCCCMACCT  
GTGGGTAATGCTCAGACCTCTCAGCCCTGTGGGTTTAATTTCTCTTTCTG  
CAGCTTAATGGGTTGGGGATGTTCACTACTGCAATAATTAGTGATGGGAT  
AGGGGAGGCAGGAGAGGATCCCGTCGACCGATGCCCTTGAGAGCCTTCAA  
CCAGTCAGCTCCTTCCGGTGGGCGCGGGGCATGACTATCGTCGCCGCAC  
TTATGACTGTCTTTATCATGCAACTCGTAGGACAGGTGCCGGCAGCG  
CTCTGGGTCATTTTCGGCGAGGACCGCTTTCGCTGGAGCGCGACGATGAT  
CGGCCTGTCGCTTGGCGTATTTCGGAATCTTGACGCCCCCTCGCTCAAGCCT  
TCGTCAGTGGTCCCGCCACCAAACGTTTTCGGCGAGAAGCAGGCCATTATC  
GCCGGCATGGCGGCCGACGCGCTGGGCTACGTCTTGCTGGCGTTTCGCGAC  
GCGAGGCTGGATGGCCTTCCCCATTATGATCTTCTCGCTTCCGGCGGCAT  
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CGAAAACCTCACGTTAAGGATTTTCTCAGCTTATCAAAAGGATCT  
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ATACAAGAGAACGGTCTACATTTACTTCAGATCCCATTTTCAGGTTAACC  
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TTGGGGGAGGATTC. FEUILLE DE REMPLACEMENT (REGLE 26) ATCTCATGT  
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[illegible]



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TTCTGCCACTTGTCC. FEUILLE DE REMPLACEMENT (PAGE 26) TGGGGG  
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CGGAAAGGACCCGCAATGATAATAATTATCAATTGCATACTATCGACGG  
CACTGCTGCCAGATAACACCACCGGGGAAACATTCCATCATGATGGCCGT  
GCGGACATAGGAAGCGCACTTCATCCATCGCTTTCTTCTGCTGCTGCCATTT  
GCTTTGTGACATCCAGCGCCGCACATTACGACGGCTTTTTCAGCGCGTTT

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Figure 6DM

GCACAAGGAA ATGCAAAGGG GCATCACTAG GGGACATGGC ACGGGGCATT  
51 CTAGGGAGCA TTGCATGGGG ACATTGCAAA GGAAATGCAA AGGGACATTG  
101 CATGGGGACA TTGCAAACAA ATTGAGTGGG AGATTGCACC GGGATGTTGC  
151 ATGGGGACAT TGCATGGAAT GTCCCACCAA CCACCCTGCA GGGTGACACT  
201 GGGACCATCC CCAGCTCTGA CCATCCCCC TTTGCTGCAG CACCACCCCA  
251 GGTCCGCATC GTCCCCATCC CCATCTCAA CGACCCCGAC ACCGTCCACC  
301 TCATCTGCCA TGT TTGGGGC TTCTACCCAC CCGCAGTGAC CATCCAGTGG  
351 CTGCACAACG GCCTCGTGGT GGCCTCAGGT GACACCAAAC TGCTGCCCAA  
401 CGGGGGACTG GACCTACAGG ACACAGGTGG CCCTGAGGGC CAGCATTGCA  
451 GCAGGGAGCA CTAAACATG TTCAGTGTGG CAATTCCAGC TTGGAGCAGC  
501 CGCTGCAGGA GGATTGGAGT GAGTTTGGGG ATGGGGATGT GGCACCCACA  
551 CCCCACAGTC CCCCACGGTT CATTGTGCCC CACGCTGTCC CCACAGGTCC  
601 CAATTTGTCC CCGGCGATGA TGGTGAAGGT GGCAGTGGCG GCCATGGCGC  
651 TGACGTGGG GTTGGTGGCA CTCAGCGCCG GGGTTTTGAG CTTCTGTCAG  
701 CGGCCACGGG GTGAGGGATG GGGATGTGGT GCTGGGGACA TGTGTGACAC  
751 CGAGGGTCTG GTGTCCAGTG TGGGGTGTAC CTCCTCATTC ATCATCTTCT  
801 GTGTGGCAGC TCCTGGCGCT GGTCCCAGTA CCCCCTCCTG ATGCGGGTTC  
851 TCACTCCAAT CCTGGTCCCC AAAATGATCC CGGTCCGAGT TCTGGTCCCC  
901 ATCCCAGTCC TGGACCCCAT CCCAGTCTG GTCCCCATTC TGGTCTTGGT  
951 CCTGGTCTG GTTCTGCTCC TGGTCCCTAT CCCTGACTCT GGTCCCGGTC  
1001 CCCATCCCGA TGCCAGTCCC AGTCCTGGTC CCCATCCTGG TCCTGCTCCT  
1051 TGGTTTGGGG ACCTCAATGA CTGGAAGTCC CATGTCCCAA CATGGGGACC  
1101 CACAGTTTGG GGTGAGGGGC TCTCACCCCA CAATAAAACC ATCTGCAGCC  
1151 CCAACCTCGC TCCAATTCTT CGTTCACAG TTGGGTGGGT CGGGCTCCCA  
1201 GTGCTCCAG CCGTNTATGT CCGTAAGCG TCGGCTCCAC TGCATAAAAA  
1251 GAAAAAAAA AAA

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Figure 7

## Séquence Génomique TAP1

(Du début de l'exon 2 à l'extrémité 3')

GGC GAG ATG GCC GTG CCC TAC ATG GGG CGA GCC AGC GAC TGG GTG GCC CGC GAG GAC AAG CTG GCA  
 G E M A V P Y Y M G R A S D W V A R E D K L A  
 GCC ATC CTG CCC ATG GTG CTG GGC CTC AGC AG GTACTGGCATAGGGGGGACGGGTGCGGGCAGGGGGCGCGCG  
 I L P A M V L L G L S S  
 GGACCCCTGACACCCCACTGCGGTACAG C GCT GTT ACT GAG CTG GTG TGT GAT GTG ACC TTC GTG GGG ACA  
 A V T E L V C D V T F V G T  
 CTG AGC CGC ACG CAA AGC CGC CTC CAG CGC GGC GTC TTC GCC GTC CTG CGG CAG AGC ATC ACC GAG  
 L S R T Q S R L Q R R V F A A V L R Q S I T E  
 CTG CGC GCC GAT GGG GCC G GTGAGGGGCACCGGGCTGGGAGGGGACACGGGGATAGGGACAGGGGTGGCACTGACGGGGCTG  
 L R A D G A  
 TCACCCGGCAG GG GAT GTG GCC ATG CGG GTG ACG CGG GAT GCG GAG GAC GTG CGC GAG GCG CTG GGC AAG  
 G D V A M R V T R D A E D V R E A L G K  
 GCG CTG AGC CTC CTG TGG TAT CTG GCA CGC GGC CTC TGC CTC TTT GCA ACC ATG GCC TGG CTG TCC  
 A L S L L L W Y L A R G L C L F A T M A W L S  
 CCG CGC ATG GCG CTG CTC ACC GCG CTG GCG CTG CCA CTG CTG GCA CTG CCC AGG GCT GTG GGG CAC  
 P R M A L L T A L A L P L L L A L P R A V G H  
 TTC CGG CAG GTATGGGCTGCTGTGTCACCTCCATGTGCTTGGTCCCTCCATGTGCTGCTGCTGCTCCCTCCATGTGCCAGTGTG  
 F R Q

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ACCACCATGTACTCATTTGCCCTATCCCATGTGCCCACTGTCCCTCCATGTACCCACCATCCTCTCTGCTGTTGTGCCCTCTCTGTGTACCGGGC  
 TGTCCCTCCACGTCGCCCATGCCCTTCCATGGGTCCCAACCATCCGTGCCATGTGCTCATTAATCCCTATGTGTGACCATTATCCCTTCCA  
 CATGGGTCTGTTCTCTGTCATGCCCTCCACTGTCCACTTCCACATGCCACCGTCCCTTATGTCCCCCTCCATCCCTCCACGTGTTCTTTG  
 TTCCCTCCCATACATGCACGTCTCCCTTCCCCAGCCCCCAATCCCTTCCCAACCGCTCCCTTATGTCCCCCTCCATCCCTCCACGTGTTCTTTG  
 CCA CAG ATG CAG AAG GCG CAG GCC CGG GCC AGC GAG GTG GCA GTG GAG ACC TTC CAG GCC ATG GCC ACT  
 P Q M Q K A Q A R A S E V A V E T F Q A M A T  
 GTG CGC AGC TTT GCC AAT GAG GAT GGG GCA GGT GCA CAC TAC CGG CAG CGC CTG CAG CAG AGC CAC CGC  
 V R S F A N E D G A A A H Y R Q R L Q Q S H R  
 CTG GAG AAA AAG GAT GTG GCC CTC TAC ACT GCC TCT CTC TGG ACC AGT GGT GTATGGGATGGGGTGGCTCAAT  
 L E K K D V A L Y T A S L W T S G  
 AGCATGGGGACGTGATGGGATGGGGCTGGGGATGTGGGACATGATAGGATAGGACTGGGGGACATGGGACATGGTGGGATAGGGCTGG  
 GAGATGTGGAGACGTGATGTAATTGAGATGTCAGGAGATGGGGACAGAAATGCCAACGGGCTGGAGGCCATATGTTGTGGAGATGGCAGGT  
 CATGGGAATATGATGGCATGGGGACTGTGGGACATAGATTGTATGGCATGGGACATCAGGATGTAGCAGGCACAAACAGTTTCAGGGGCTCT  
 GGGGCAGGAGGATGCAGTGACGTGGGAATGGGGATGGGGCTCCAGGACACTGGGACATGATGGCATGAGGGGACATAGCACAGAG  
 ATAGCACAGCTGTGGGACACTGGGACAGGGGGGACATTGACAGACAGGAAGGTGACAGAGTGGTCTGGGGACTCAGAGTCCCAGGGGGGA  
 GGTGTCCCTGGTGACCTCATGGCATCCTCAG TTC TCA GCC CTG GCC CTG AAG ATG GGG ATC CTC TAC TAT TAT GGG  
 F S A L A L K M G I L Y Y G  
 GGG CAG CTG GTG GCC GCG ACC GTC AGC ACT GGG GAC CTC GTC ACC TTC CTC CTC TAC CAG ATA CAG  
 G Q L V A A G T V S T G D L V T F L L Y Q I Q

FIGURE 7 - SUITE 1

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Figure 7

TTC ACT GAT GTC CTG GAG GTGAGCCTGAGAGGATGCCCATATCCGATGTCCCCATGTCTCCCTGCCACAGTCACAGTGTGTCA  
 F T D V L E  
 CAGTGTCCCTGTGTTCCCTACATCCTCCCTGCTGTGTCTCCAGGGCCAAATCGAGTGTGTCCCCATGCCCATCCATGTCCCTGTGTCCCCACG  
 TCTAACCCCTGTGACCCCTGCCACATCCCTGTGTCACTCCTCTGTCTCCCCATACCTACCCCGTCCCTGTCCCTATGCCAATCCCACTGTGT  
 CCTCTGGTCCCCATGTCACCATGCCACATGCCCTTGGCCCTCCTGGCCACGTCACTAGCTGTCCCCAG GTC CTG CTC GAC TAC  
 V L L D Y  
 TTC CCC ACA CTG ATG ANG GCT GTG GGC TCT TCG GAA AAA ATC TTT GAG TTC CTG GAC CGG GAG CCA CAG  
 F P T L M K A V G S S E K I F E F L D R E P Q  
 GTC TCA CCC TCA GGG ACA ATG GCA CCC GCT GAC CTG CAG GGC CAC CTC CAG CTG GAG GAT GTC TGG TTC  
 V S P S G T M A P A D L Q G H L Q L E D V W F  
 TCC TAC CCT GGG CGC CAG GAA ACC CGT CCT CAA GTGGGCACAGACACAGCCAGGGGACACGGGGTGTGGTGGGACA  
 S Y P G R Q E T R P Q  
 GCGTGACAGGTGTGGAGCACAGTGGGTGATTCAGGGACATGGATGTGATGGACAGGGTGTGAGGATATGAACAAAGGAGATACATGGAGG  
 GGGTGTATGGGACACTGGAGAGGGACATGAGATCATGTTATGAGGGCGCGGGACATGSCACATGTGGGTGTGSCACTGGGACAT  
 GATGAGTGACACAGAGACATGGTGGGAGGGCATGGGAATGTAGAGGCCGTGGTA  
 GGG GTA TCA CTG GAG CTG CGC CCC GGG GAG GTG CTG GCA CTG GGA CCC CCG GGC GCA GGG AAG AGC  
 G V S L E L R P G E V L A L L G P P G A G K S  
 ACT CTG GTG GCC CTC GTG TCC CGC CTG CAC CAG CCC ACG GGC CGC CTG GGC CTG CTG GAT GGC CAC CCC  
 T L V A L V S R L H Q P T A G R L L L D G H P  
 CTC CCC GCC TAC CAG CAC TCC TAC CTG TGC CGC CAG GTGAGCAGCCACATGTCCCCATGGCTCCTGTGTGTCCCCCTG  
 L P A Y Q H S Y L C R Q

FIGURE 7 - SUITE 2



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TGTCTTGATATCAGCAGCATCCTCATTTGATCACCAGATATCTGGGTCCCAGCCATCACCACACACCCCTGATGTCTCTGCCATATCA  
 CCACTGTGTCCCCTGCAGTGTCCCGGCAAGTCCCAACCATCTTGTGTCCCACCATCCACCATGTCCCAGATGTCCCTGACACAT  
 CCCCAGGCATCCCCACCGCTCCACTGCCACGTTGCCCATGTTCGCCAGCTGTCCGCCCTCCACTGCAG GTG GCC GTG GCC CCG CAG  
 V A V V P Q  
 GAG CCG CTG CTT TTT GCC CGC TCA CTC CAC GCC AAC ATT TCC TAT GGG TTG GGG GGC TGC AGC CGG GCA  
 E P L L F A R S L H A N I S Y G L G G C S R A  
 CAG GTG ACA GCG GCC CGC CGG GTG GGC GGC CAC GAC TTC ATC ACT CGC CTG CCC CAA GGC TAC GAC  
 Q V T A A A R R V G A H D F I T R L P Q G Y D  
 ACA G GPAAGCTGTCCCTTTCTGTTCGGGTCCCTCCATGTCTCCCTCCAGCCTGACCCCGCTCGTCCCGCAG AG GTG GGC  
 T E V G  
 GAG TTG GGA GGA CAG CTC TCC GGG GGG CAG CGG CAG GCG GTG GCC ATT GCC CGT GCA CTG CTG CGG GAC  
 E L G G Q L S G G Q R Q A V A I A R A L L R D  
 CCC CGC ATC CTC ATA CTC GAC GAG CAC ACC AGC GCC CTG GAC AAT GAG AGC CAG CAG CAG GTGGGATGTC  
 P R I L I L D E H T S A L D N E S Q Q Q  
 CCCCACGTCCCGGTGTCCCCACATCCCCCTGAGCCCTGTGTTCCTCCATTCACGCTAGGTCCCATGGTCCCTGTCTCTGGTGTCCC  
 CTTATCTCCACTCTGGTGTCCCTCGGTCCCTGGCAGTGGGTGAGGAACATCCCCCTGAACCGTTTCTCTCCACAG GTG GAG CAG  
 V E Q  
 GAG ATC CTC GCA GCC AAA GGG TCG GGG CGT GCA GTG CTG ATG GTG ACG GGG CGG GCA GCC CTG GCG GCG  
 E I L A A K G G S G R A V L M V T G R A A L A A

FIGURE 7 - SUITE 3

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Figure 7

CGG GCA CAA CGA GTG GTG GTG TTG GAG GGG GGA GAG GTG CGG CAG GAG GGA CCC CCC CAC GAG GTG GTG  
 P A Q R V V V L E G G E V R Q E G P P Q E V V  
 CGC CCC GTC AGC CTT NTT GCG GGA CTG GGG ACA ACA AGG GAG CAC CGG GGG AGG GGG ACA GAG GGA TAG  
 R P V S L ? A G L G T T R E H R G R G T E G \*

CGGGAGTTTGGATGGGGAGGGGCGGGGTGGTGGGATGTGGGATGGGGACACTGCCGTTGGGGACACTGAGGGTGGAGGTGGGGACAC  
 CGGGGACGACACAAAGGACCAAGAGCTGTGCCCTGGGCACATGGATGCCGAGCCGGCGCGCTCCGGTACCGCTGCTGTACGACACACA  
 ACGGCCACAGCATGGACTGCAGTGCCACTGAGTGCCACCAGGGCGGGGTGGGACACAGAACTGGGAATAAGCCCGCATGTTTGT

FIGURE 7 - SUITE 4

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Figure 8

TAP2G

-213  
CGCCATACATTTTGGCCCTGTCTATGCACGGTGNFATGGCCGACCTGGCCNTCATGTTGGCCCTGGCCCCANTTCTTCCAGCACTGGCCCA  
TTGGGCTGGTGGC -107

-106  
TCCTGGCGGAGGCCGGGCTCGCCCTCTCTGCTGGTGGGGGGGGCGGGGACGCTGCTGGCCCCCAGGGACCCCGTGGGGCTGCAGTGTCTGCT  
AGCATGGCCCCGCC 0

+1 ATCTTCTGACCTACGGGGCTATGATGCTGCTGGAGCTCCCGGTGCTGTGSCC ATG GCA ACG CCG TC  
TGG CTG GTG CTG ACC CAC +93 5'UT

W L V L T H M A T P S

+94 GGG ACA GCT GTG GTG GCA TTG CTC ACC TGG AGC CTC CTG GTC CCC ACT GTG GCC ACT GGG  
GCA AAG GAG GCA AAG GCC TGG +174  
G T A V A L L T W S L L V P T V A T G  
A K E A K A W

+175 GTG CCC CTG AGG CGG CTG CTG GCG CTC GCG TGG CCC GAG TGG CCG TTC CTT GGC TGT GCG  
TTC CTC TTC CTC GCA TTG GGT +255  
V P L R R L L A L A W P E W P F L G C A  
F L F L A L A

+256 GCA CTG GGT GAG ACC TCA TTG CCC TAC TGC ACC GGG AGG GCT GTG GAT GTC CTC CGC CAG  
GGG GAC GGC CTC GCC GCC TTC +336  
A L G E T S L P Y C T G R A V D V L R Q  
G D G L A A F

+337 ACC GCT GCT GTC GGC CTC ATG TGC CTG GCC TCT GCC AGC AG  
GTAGGACCCCATCCCTCCACAAACCCCATCCACCTCTGGTGGTGTCT +429  
T A A V G L M C L A S A S S

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+430  
GGTGGGTTTGGGGTCTCTGTCCATATCTGGGGGTCTGATGGGTTCTGGGCACCTCCACTGACCCCTTTGTGATTGTCTGAAGGGTTCTG  
GCTCTCCATTGACCC +536

+537 CTGATGGGTTTGGAGTCGGCCCCCAATTCCTTCCAG C TCG CTG TTT GCC GGC TGC CGC GGT GGC CT  
TTC ACC TTC ATC AGG TTC +624  
F T F I R F S L F A G C R G G L

+625 CGC TTC GTC TTG CGC ACC CGC GAC CAG CTC TTC AGC CTG GTG TAC CGG GAC CTC GCC  
TTC TTC CAG AAC ACC ACA GCA +705  
R F V L R T R D Q L F S S L V Y R D L A  
F F Q N T T A

+706 G GTACAGACTGGGGGCACTTTTGTCCCTGTCCCAACCATACCCCGAGCTCACCCTACTCACTCCACAG CT GAG  
TTG GCC TCC CGG CTG ACC ACC +828  
L A S R L T T A E

+829 GAT GTG ACG CTG GCG AGC AAC GTG TTG GCA CTC AAT ATC AAC GTC ATG CTG AGG AAC CTG  
GGG CAG GTG CTG GGG CTC TGC +909  
D V T L A S N V L A L N I N V M L R N L  
G Q V L G L C

+910 GCC TTC ATG CTG GGG CTG TCC CGG CGC CTG ACA ATG CTG GCA CTG CTC GAA GTG CCG CTC  
GCC GTC ACC GCA CGG AAA GTC +990  
A F M L G L S P R L T M L A L L E V P L  
A V T A R K V

FIGURE 8 - SUITE 1

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Figure 8

+991 TAT GAC ACC CGG CAC CAG  
GTGATAGCAGGGGATGGATGGTGGGTGACAGGGATGGAGGCAATGGCAATGGGATGGGAACAGTGGGAGTGGGGAT +1091  
Y D T R H Q

+1092  
AGTGAGGTGGGATTTGTGGGTGACGGGTGGCAGGGATGAGGGCAGCTGCAATGGGATGGGAACAGTGGGAATGGGAGAGCAGGATGGGGA  
CATGGGTCCACACA +1198

+1199  
GCRAGGATGAGAGGATGGAGAAGATGGAGCAGGAATGGAAGTGGGATGGCGNCTACTTGGCCATCCCATGGGTGCTGACACCCACTGTCC  
CCCCAG ATG CTG +1302

M L  
+1303 CAG CGG GCC GTG CTG GAT GCA GCA GCC GAC ACC GGA GCA GTG CAG GAG TCC ATC TCT  
TCC ATT GAG ATG GTA CGG GTC +1383  
Q R A V L D A A A D T G A A V Q E S I S  
S I E T V R V

+1384 TTC AAT GGC GAG GAG GAG GAG CAC CGC TAC AGC CAG GTG CTG GAC AGG ACC CTA CGG  
CTG CGG GAC CAG CGG GAC ACA +1464  
F N G E E E E H R Y S Q V L D R T L R  
L R D Q R D T

+1465 GAG AGG GCC ATT TTT CTC CTC ATC CAG CGG  
GTGAGGCTGACACAGGGGACACCCCTGTGTTCTGGTGGGATCGGACATCCCGCTGAGGCCCAT +1561  
E R A I F L L I Q R

+1561 CCCCACAG GTG CTG CAG TTG GCT GTG CAG GCA CTG GTG CTA TAC TGT GGG CAC CAG CAG CTC  
CGC GAA GGG ACC CTC ACT +1641  
V L Q L A V Q A L V L Y C G H Q Q L  
R E G D L T

FIGURE 8 - SUITE 2

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+1642 GCC GGC AGC CTC GTC GCC TTC ATC CTC TAC CAG ACT AAA GGT GGC AGC TGC GTG CAG  
GTGAGGTCAGGACGTGCTCTCTGCCACGG +1729  
A G S L V A F I L Y Q T K A G S C V Q

+1730  
GATCCCCATGACTGTGGCCACATCCCCGTGTCCTGGGTGCTGTGCTGGGGTCAATCCCCATGTCCCTATCCTGGGTGCTGTG  
CATGCAG GCA CTG +1834

A L

+1835 GCG TAC TCC TAT GGT GAC CTT CTG AGC AAT GCA GTG GCC GGC TGC AAG GTC TTT GAT TAC  
CTG GAC TGG GAG CGA CCT GTG +1915  
A Y S Y G D L L S N A V A A C K V F D Y  
L D W E R P V

+1916 GGT GCT GGT GGC ACC TAT GTG CCC ACC AGA CTG CGG GGC CAC ATC ACC TTC CAT CGG GTG  
TCC TTC GCC TAT CCC ACT CGC +1996  
G A G G T Y V P T R L R G H I T F H R V  
S F A Y P T R

+1997 CCT GAG CGC CTC GTC CTG CAA GAT GTC ACC TTC GAG CTG CGC CCC AGT GAG GTG ACG GCG  
TTG GCG GGG CTG AAT GGC AGC +2077  
P E R L V L Q D V T F G L R P S E V T A  
L A G L N G S

+2078 GGG AAG AGC ACC TGC GTG GCA CTG CTG GAG AGA TTC TAT GAA CCT GGG GCC GGA GTG  
CTG CTG GAC GGG GTG CCG CTG +2158  
G K S T C V A L L E R F Y G P G A G E V  
L L D G V P L

FIGURE 8 - SUITE 3

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Figure 8

+2159 CGG GAC TAC GAG CAT CGC TAC CTG CAC CGC CAG  
 GTGATGGGTGGGGGAATGTAGCTGCACTGAACANTGCTGGGGCTGACCTCTGCCCTGG +2254  
 R D Y E H R Y L H R Q  
 +2255 GGCAG GTG GCA CTG GTG GGG CAG GAA CCC GTG CTC TTC TCT GGC TCC ATT CGG GAT AAC  
 ATT GCC TAC GGG ATG GAG GAC +2335  
 V A L V G Q E P V L F S G S I R D N  
 A Y G M E D  
 +2336 TGC GAA GAG GAG GAG ATC ATA GCA GCT GCA AGG GCT GCG GGT GCT TTG GGC TTC ATC TCT  
 GCA CTG GAG CAA GGC TTT GGC +2416  
 C E E E I I A A A R A A G A L G F I S  
 A L E Q G F G  
 +2417 ACT G GTGAGTCTGGGAGCAAGGGGGGACCCGGGTGTCTGACCCCACTCATCCCACTCATCTGCGAG AC ---  
 GTA GGG GAG AGA GGG GGG CAG +2511  
 T  
 G E R G G Q D  
 +2512 CTG TCA GCG GGG CAG AAG CAG CGC ATC GCC ATC GCC CGC GCT TTG GTG CGG CGT CCC ACC  
 ATC CTT ATC CTC GAC GAA GCC +2592  
 L S A G Q K Q R I A I A R A L V R R P T  
 I L I L D E A  
 +2593 ACC AGT GCT CTG GAT GGG GAC AGC GAT GCA ATG  
 GTGAGCACTGAGCAGTGGGTGGGGAGGGTCTG?CCCTGCAGTGCATGCTGATGGGAGCTG +2688  
 T S A L D G D S D A M  
 +2689 TGTCTCCTACAG CTA CAG CAG TGG GTG AGG AAC GGA GGG GAC CGG ACG GTG TTG TTT ATC ACC  
 CAC CAA CCA CGG ATG CTG +2769  
 L Q Q W V R N G G D R T V L F I T  
 H Q P R M L

FIGURE 8 - SUITE 4

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+2770 GAG AAG GCA GAC CGC ATT GTG GTG CTG GAG CAT GGC ACG GTG GCT GAG ATG GGG ACA CCC  
 GCC GAG CTG AGG ACC CGC GGC +2850  
 E K A D R I V V L E H G T V A E M G T P  
 A E L R T R G

+2851 GGA CCC TAC AGC CGG CTG TTA CAG CAC TGA  
 GAACCATGGAGCAGCTGGAGTGGCATGGATGGGATATGGGGAGCAGTGAAGTGGCTTGGCTTCCAGC +2947  
 G P Y S R L L Q H \*

+2948 TGCAGGATGGGATGTTTGGGATTGTGTGGAAATAAAGTGGAGATGCTTTGT  
 +2999 3'UT

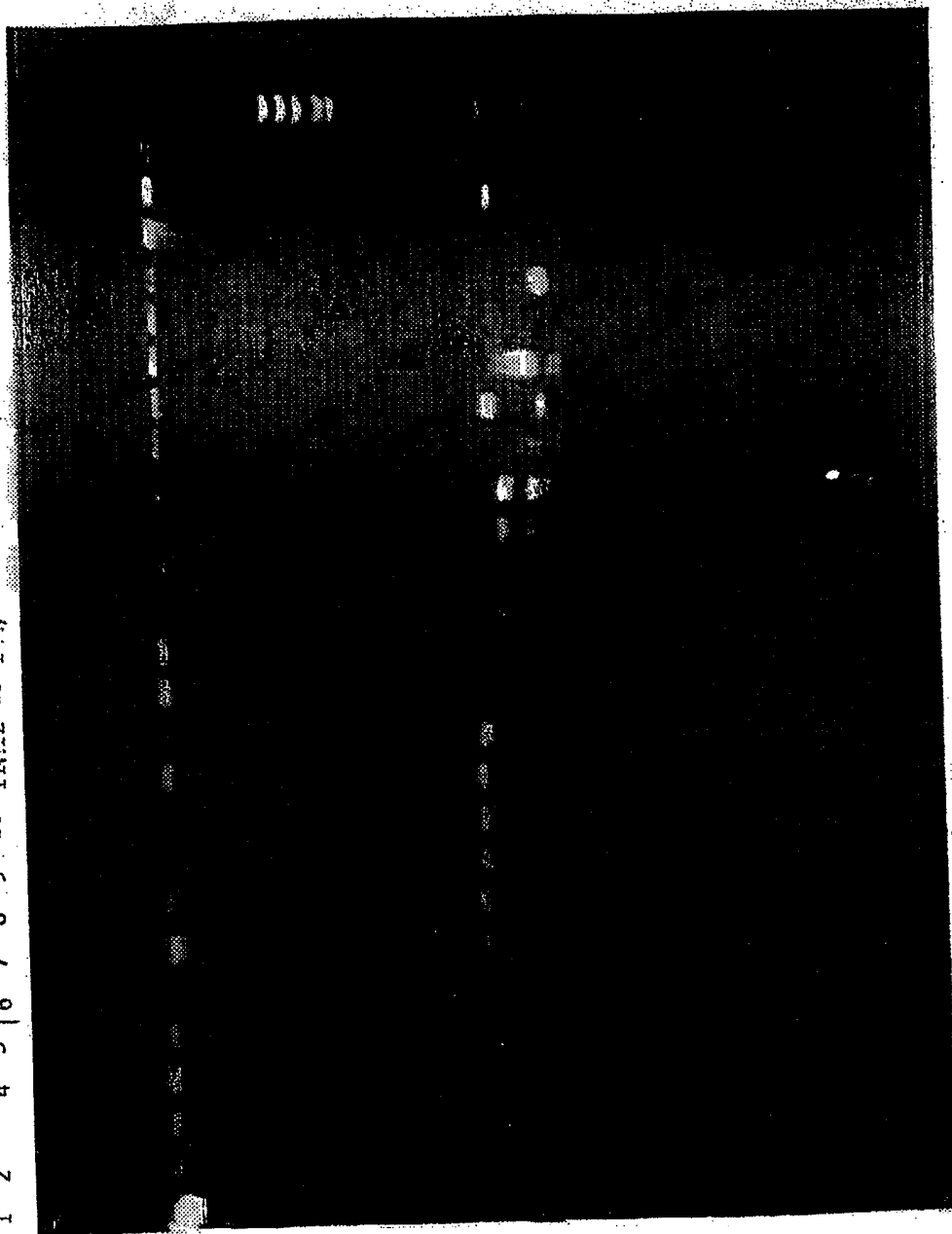
INTRON 2-3 : EF23(1B-1R)3R  
 INTRON 3-4 : EF23 2(1)  
 INTRON 4-5 : EF23 352H CON  
 INTRON 5-6 : EF23224RS  
 INTRON 6-7 : EF23(5B-5R)1R  
 INTRON 8-9 : EF23277B CON  
 INTRON 9-10: EF23 43RSR  
 INTRON 10-11: EF23 43RSR  
 INTRONS 1-2 ET 7-8 INEXISTANTS CHEZ LE POUET

FIGURE 8 - SUITE 5



FIGURE 9

B4  
 1 2  
 B5 B7  
 4 5  
 B12  
 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 23 24 25  
 B13  
 B14  
 B15  
 B21  
 BX  
 27



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A5FIN.txt

GTCCCTATTCCCATTGTGTCTCCTCACATCTGCCATCTCTTCTGTCCCCAT  
CTATGCTTTGTGCCCCCATCCCTTACCCCATCCCCACGTGTCCCTGTGG  
TGCCACCTCCACACGTGTCCCCGTGTCCCCACAGCGGGGCCGTGGCGCAA  
TAACACTGTGATGTGGCGCTGTGCCGGGACGGAGCGACGGCGCTGCCCA  
TCCGTGCCACGTGCCAGCAGAGGGGACAGCGGGTGACGACGGCCGGGGG  
TGCCGAGACGCCTTCTTGCAGTGTGTGAGGTGGCACAGAATCTGCGGCG  
GAAGGGACAGCGCGGGGGGTGGCACGGGGTGAGTGTGACGAGTGTCCCC  
GTAGAAATGGGGACCCCATTTGGTGTGGGGAGGTTTGGATAAGGGGTCCCC  
ATGGGTGGTGGCACATGGGGACATCCCATAGCCTGGGATCCCATGGTTGG  
GGCCATCCCGTACCTGGGATCCCCACATGGGAGGATGTCCCCCGCTGTCC  
CCATGGCAGTGATGGAGGCACAGCTGGCAGAGCAGCTGTTGGATGATGAT  
GAGGACGTCCCCACGAGGAGCTTCTTCCCTGAGAGCTGGCTGTGGCGACG  
CATCCATGTTGCTGGCACTGCACGGTGTGTCCCCGTGTGTCCCCATGTCC  
CCATGTCCCCATGACTTTGTGTCCCCGTGTCCCCATCTCCCCATCTCCCC  
AGGCTCTCAGTGTGCTCCCTGACTCCATCACTACGTGGGAGATTGAGGC  
AGTCGCCATCGTCCCTGGACATGGTGAGTGTACCCCCCTCCAATGGCCCT  
GCAGTGTCCCCCTGACATCCCCCTCGTGGTGTCCCCATGTCCCCCACGTC  
CCCAAGTTCTATGGTGTCCCCATGTCCCCCTCTCCCCCTCCCCCGGA  
ATGTCCCTGTGTCCCCGTGGTGTCCCTGCACTGCCCCGCACTGATGAGGT  
CCTGGCAGGGCTGTGCGTGGCGGAGCCGACGGGTGACGGTGACACAGG  
ACGTGCGTGTGGCGCTTTGGCTGCCCCCAGCATCCGGCCCTAGAGCAG  
ATGCAGCTGCAGCCTCATCCACAGCAGACTGCCCCGACGATCAACGT  
AAGCCCTATAGAGACCCCATAGGCACCCAGAGATACCTCTTTCCCTCTA  
ATAAATAACCACTTTGCTTCCAATAGATAACCCTCCTGCCCCATAGGTACC  
CCTGTGCTCCATACTTGCCCTGCCACAGCATAACATACCCCTTTCCCTCCA  
ACAGATATGCGTTGCCCCATAGATACCTTCTTTCTGCCCTATAGATAACC  
CCTCATGCCCCACAGATTCCCGTTTCTTTCAATTGGTACCCCTGCCCC  
TCATATATCCCCCTTACCCACGGATACCCCTTAGACACCCGGTACCA  
CTTCTGCCCCATGGATACCCCTGTGGCACATAGATAACCGCTCTGCCCC  
ACAGATACCCCTTCTACTCCACTGTCCCACAGCCCCACTGCCCCATG  
GCCACCCATAGCCTGGTGGCATCGGGTGACAGTGACGGTGATGCAGGTGA  
CGGTGACACTGTGCGCAGTGGAGGGGGTGTGCGCGGCGCTGGATGGGGTC  
CCCCAGATGCTGGAGCTGCCCCGGGGAGGGCAGTGGCTGCACCCCTCAC  
TCTGGTGGCCCTCCACCCTGGGGACATCCCATCACCATCACCGCCCGG  
GGCCATGGGGGCTGGGGGACCGTGTACCCGAGTCCCTGCATGTCGAGGTG  
AGATCAGTGGGGTCCCTCCAGTCACTGGGTCACTCTGGGGTCCCTTA  
AAGCCCTGCGACCTCCTGGACATTGTTGTCTTGTGAGCCTGCGGTACCC  
CTGAATACTGGGGCTGTCACTTTGAGGTTTATGGACACCATGTCCCTGTG  
TCCATGGTGGCCCTGGACATGTTGGTCTTATGGGATCTGGGGACATGGG  
GTCTTGGTGGTCTGGATACTGCAGTTGTCTTTTGTGGACACTATGTC  
CCCATGTCTTGGTGGGAATGGTGTATCCATTCCCGCAGCTGAGGGAG  
AGCTGCACCTGGAGGAGAGCACCTACATCCTGGACGCAGATGGTGGGTGT  
GAGGACTGGGGGACACTGGGGAACTGGGGACGTGGGGCCGGACCCTGTG  
GTGTGGTGTCCCTACAGATAAGCGGAGCCGGAGCCTGAAGCTGCCGGGGG  
ACGTCCCTGCAGAGATCGTCCCTGATGGGGACTTCAGCATGAGCATCCGT  
GTCAGTGGTGTGTGGGGATGGGGACATGGGGTGGGGACATGGGGGTGGGT  
ACTGGGAACGTGGTGGGGATGTGGTGGTGGGCATAGGGGACATGGGGACA  
TGGGAGGACATTTGTGGGGACATTGATGTCCATCCCTGATCATCTCTCT  
GTCCCTATGTCCCCATACCCATGTGTGTGGCCATGTCCGCACGCTGTGCC  
CCTGTGTGTGTCCCCCTGGGTGTCCCCACATGTGCTCACATCCTTATTACA  
TCCCCACATCTCTG. GTACAACCCCGTGTGCCCTGATGTGTGCCCTCC  
ACACATCCCCATGGGTGTCCCAATGTTCCCATGTCCCTCTGCTCATCCC  
ATCCACATCCCCATGCCCTATGCCCTATGGGACGTTGGGGCATTTTCCA  
TCCTATCCCCATGTCCCCATGTCCCATATCTCCATACCCCTGTGACCCCA

FIGURE 10

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TATCCCTGTCCTTCAACTCCCCTCCCATCCCCACACCATCCCCATGTCTT  
CTGTCCCCACACCATCCCCATATCCCCCTGTCCCCCTGTCCCTGTCCCA  
GGCCGGGTGCCGGCTGGGCACTGCAGGGCGCTCTGGGGATAGGGGACTC  
TCTGCTCCGCTCCCCCGGGCTGTGGGGAGCAGTCCCTGATGTCAATGG  
CACCCACTGCTGCTGCTCTGCGCTTCTGGATGAGAGCGAAGGGTGGGG  
CAGCTGCCCCCAGGGCACCGACAGCGCGGCCTCAGAACCCTGCAGCAGGG  
TGAGCTATGGGGCAGGTTGTGCTTTATGGGGTGGGCAATGCTTTATGGGG  
TGTGCAGTGTCTCAAGGGATGTGCAGTGTTCATGGGGGATGCAGTGGGG  
TTTGATTTGATTTGATTTATGGGTTTGCAATTTCTCCTCCGAGGATTGCAT  
CTCTCTATGGTGTGTTGCAATGGGATGTGCAGTGTCCAGGTGGAGGTGCA  
GAGCCCTATGGGGGTGCAGTGTGTGTAGGGGATGTCTGTGGTGTCCCCA  
ATGGTCTCTGATGTCCCCACAGGCTTCGAACGGGTGCAGAGCTTCCGCAA  
AAGTGACGGCTCCTATGGGGCATGGCTGCACCGGGACAGCAGCACCTGGT  
GAGGGGAGCGGGGATGATGTGGGGACATGGGGATAGTGAGGGGATGTGGG  
GATGCTGGGGTATGGGGATGTGAGGACATCATAGGGACATGAGCGGTGGG  
GCCATGTGGATTTGGGGACGTGGTGACACGGTGTCTGGTGCAGGCTGAC  
GGCACTGGTGTGCTGCGTGTGCTGGCCCTGTCCCGGCCCTATTTGCCAGTGG  
CTGCCAGCGGCCCGCTGCGTCCCTGCGGTGGGTGCTGGGGCAGCAGCGC  
CCAGATGGCGCCTTCTTGGAGCACAGGGCTGTGGTGCACCGTGAGATGCA  
GGTGGGTGACACATCACTGCTGTGTGCAATGTCCCCATGCAGGATCTCCC  
CCTGCAATGTCCCCTGAAGGTCCCTGCAGGCTGACCCACATTACACTGT  
GTCACTCACGTGTCCCGTGTCCCCAGGGTGGTGTGGCAGACCCCGGCC  
GGAGGCCACCGTGTGCTGACGGCCTTCGTGGTGGTGGCCCTCCATGGTG  
CCCGCGCTCTGCTGCCCCCGGACAGCCCTGAGCTGCCCTCCTGGTGAGT  
CCCATGTCCCCACCCCTGTGTCTTGGTCTCATATCCATGTGTCCCTGT  
GCCCCATCCCCAAATCCCCACATCCCCATATGTTCCCATACCCCTGCTG  
TGTCCTCCAGTGTTCCTCCCGTCTTTTCAATCTCCACTATCCCCGTATTC  
CCATATGTCCCCCTGTCCACAGTGTCCCTCATCCCTCTGTGTCCCCCT  
GTCCCCCAGTGTCCCCCAGTCCCTGTATGTCCCCATGTCTCCTAGTGTC  
CCCCATGTCCGTGTCTCCAGTATCCCCATGCCTCCCCGTGTCTCTTCA  
TGCCCCACACTCCACGTCCCCACACTCCATGTCCCACTGCCACAGGACAA  
ATCCCTGTCCCGGGCCTCCACGTTCCTCCGGGGCCGCTGGAGCAGTTGG  
GGACCTATGGGACAGCCATTACATCCTATGCATTGGCACTGGTGGACACC  
GCTCCTCCGGGGCCGATCCGGCGGTGGAACGTCTGCGGGGCATGGCCCG  
GAGCGCCCAACGGTGCCTGTCTGTGTCCTCCCATGGGGTGGTGGCACCTCT  
GTCCCCATGGCTGCCTCCTGGACCCCTCTGTCCCTCCTTCAGATTCAT  
CTCATTCGAATCCTTCAATTTTATTCTCCCTCAAACCTTTCTTTTGT  
TTCTTCACATTCATTCTTCAATTTGTTCTCCTGATTAATTCTTTAAATTA  
TTCAAATTTCTTCTTCAATTTTGTCTCCTGATTAATTCTTTAAATTA  
CTCTCGATCAAGTTCTGCAGATTCGTTCCACTTCGGATGGATTCTTCTCC  
AAACTGTTCTTCAGATTCATCTCCTTCAATTTCTGTTCTTGTAAATTA  
TTCTTTCAGAGTGATTCTTCAAACCTTTCTTTCATGTTCTCTTCAAGTCCA  
TTCCCTGCACTGACTCCGGGTGCTCAGGACCCCCCGTGACCCCATATGA  
CCCCATATGAACCCCCCATGACCTCCACAAAACCATATGACCCCGTGACC  
TCCCATGACCCCTCATGACCCCATATGACCCCATGACCCCATCCCTGT  
GCAGGTGGCCGTGCAACCTTCTGGCCATCCGGTGGCCCCGACGCCACGGT  
GGAGGCGACGGGTTACGCCCTTCTGGCACTGCTGCAGAGCCGCGACATCG  
CCGGGGCTGCGAGGGCGGCACGGTGGCTCCGACAGCAGAGCAATTACGGG  
GGTGGCTTCCACTCCACGCAGGTGGGTGGGGGTCACTGACCCCGGGTG  
CCTCGGGGTGGGGGTGATTTGATCCCCAGGTACCTCTTGGTGGCTGTGT  
CCCCAACCTGCTTGGTGTTCCTCGAGGACACGCTGGTGGCCCTGGAGGCG  
CTGGCCCAGATGTGGCTGCACTGGGGCCGTGGGAACACAATGGGGCTGAA  
CCTGGGGCTCTCCTGGCCGGGGGTGCCCGGGGGAGGGCTGGTGGCACTC  
AGGTTATGCTGAAGCCGGGGCTGGAGCCGCTGGAGCAGGACCTGCAGCTG  
GGGACATGGCGGGATGTGGGGACACGAGGGATGTGAGGACATGGGGACA

FIGURE 10

SUITE 1

TGCTCTGGACTTGGTAGGATGTAACATGAAGACACTGGGGACATGGTAGGA  
CATGGGGGACATGAGAACACGGGATGTGGGGGACATGGTAGGACATGATG  
GACACAGGGCTTTGGGGTCCTTGGGGTCCTCGCTCTGTCCCCATGTCCCCA  
GGTGCCTCTGGGCAGCCAGTGACAGTGACAGGTGGAGGGACACGGCGAAG  
GGACGCTGACGGTGGGTGGCTGCATGGACATTGGTGTCTCTCCAAGACC  
GATGTCCCCCTCACAACTCCCCTCATGGTGTCCCCTCATGCTGCCACGGT  
GTCCCCTGCTGTCCCATCATGGTGTACGCTGTCCCCAGGTGCTCCGCCA  
GTTCCGCCTGCTGTACCTCCGAACGCCACGTGCCAGGCGCTGCACCTGG  
AGGTGGCCATCACCGGCCCATCCTGTACCATGGTGAGGCCCCACCCAAA  
GGCCCCGCCCTTTTCTCGCGGGGGCGTGCCCTCAACCCTGTTTTGC  
ATATCCCAACCCCCAGCAGATGAGGACTACGAGGACTACGAGGACTACGA  
GGAGGCGGAGCCTAAGGAGGGGGAGGAGCCTACGGAAGGGGACGTGCCCG  
TGGAAGGGGCGGGGCCAGCAGATGACCCCGCCCCCTCAGCCCCGTGTCC  
TTATGGGATGCCCGTAAGCGGCAACGCCGACGACACATAACCCTGCCCA  
CGAGGTGGCTTCTTGGTCTGCTTCCGGTGAGGGGCGGAACCTTCTGTCC  
CTGGGGGCGGGTCTTCTGCTGATGGGCGTGGCTTATTGCTGAGGGGCGT  
GGCCTGTTGTAGGCGGAGCCCAGGGGTGGCACTGACTGGGATGGCGGTGG  
TGGAGATCACTCTGCTCAGTGGCTTCTCACCCCATAGAGCTGACCTGGAC  
AAGGTAGGGGCCCAGGGGGACTTGTGGGACATGTTGGGGGGTTGAGGGGA  
GTTATGGGGTGTGGGGTTTGGGGGTGTTGGAGTTGTTGAGGTGGCAGAAT  
GTTTGGGTTGGAGTCATGGGATATGGGGCTATTGGGGTTTGGGGTGTG  
TGATGTTGGGAAACATTGAATTGGGGTTGTTGAGTTTGGGGTGTG  
TGTGCGGGTGACAGCTGCAGCTGCTGGGTTGGAGTATTAAGGTGTTGGG  
ATGTTGGGGTGTGGATGGCTTGGATGCGGGTGTGGGGTGGGCACGTAT  
CTGGGTGCTGCTGTCCACAACAGCTGCGGGACGTGGTGGATCACTGGAT  
CAGTCACTATGAGTTGGAAGGAAACAGTTGGTGTCTATACCTGGATGAGG  
TGTGTCTTCCCGTGTACCCCTATAACCCAGTGGCCCCATGTTCTCATAT  
CCCCCATGTCCCCGTGTCCCCACACCATATCCCATTCTCCCCACACATCC  
CCGTGTTCCACCACGTGTCTCTCATTCTGTCCCTGTCCCCAGGTCCCCC  
CGAGCGGTGACAGCTGCTCAGTTTGGGGGCCACCCAGGACGCGGCTGTGGGT  
ACATGCAGCGGCAATGGCAGCCATCTATGACTACTATGAGCCTGGTGGG  
TGGGGCCTTCAGTGGGAGGGGCTAAATGGGTGGTGGTCTTCATGGGTGT  
GACCATTGGAGGAGGCGTGGCCGATCTGACCCCTCCATGCCCCATCCAGG  
ACAGCGCTGCACCGTCTTCTACAACGCCCCCAAAGGAGCAGCACCATCG  
CCACACTGTGCTCCCCAAAATCTGTGAATGCGCCCAAGGTAGGACCCCA  
CTGTGACTCCATATGTAGGGCCCCCATCCAGTGAACCCCCACATCTCTCT  
CCTAATTTTGAAGATCTGGGGGTGAAATTATGGGGTTTATAGGGGAGCG  
TGGTTGAGTGACATGCAGGACATGGAGGAACCCACACCAAGAACCTTGT  
GTTTTGGGTCCCTGATGATGTTGGGAGATCCTATTGATGTTGGTGGTCCC  
CAGGGGGGTGTCCCCAAGCCCAAGGAGGACACAGGAGGTGACAGCTGAT  
GACCGCCATGACTTTGCCTGCTACAGCCCCCGCGTGGACTATGGTGGAT  
CCCAAATCACTGCACCTCAAACCTGACCCCAAATTGGCTGCATCCCGAAC  
CCCAACTGCCCTAAATCCCATCTGCTGCCCTGAGTCCCACAGCTGCACA  
CTGTACCCACAACTGGCCCCCTGAAGCCTAAAAACATTACGAGGATTTT  
GTAGTTTCTCCCTGTACCCAGTTGTCCCTCTGACCCCAAGAACCCAC  
AGCTGCCCTATGCTGTCCCTGCCCCGCCATAACTCCTCTGATACAATAAC  
CCCCGTGACCCCATCTTTATGACCTCCATGACCTTTGACCCCGAGCACTG  
GTGGTTCCGGGTGCTGTCCAGAGTGAGATAGGGGCTTTTGTGGCGTTTGA  
GACGGAATCAAGGAGGTGCTGCTTGAAGGTGAGACTGAGGGTAGTGGGA  
CGGACTGGAAGGTGAGAATGGGAGCACTGGGAGAGGACAGGGAGTACTGAG  
AGGGACTGGGAATGACTGGAAATTGAGACTGGGTGGACTGGGAACCTCTGG  
TAGAGACTGAATGGGTATACTGGGAACACTGGAAGAAGTTGTGGGATGAG  
AAGAGGATGCTGGGATAGCAGACCCCCCTTGTGCTAGGGGGGTCTCT  
CAGCCATACTGGCACAATATGAGAGTATACTGGGTGGTACTGGGAAGCT  
GGGAGGACTCATACTGTTCTCTACTGCTGCAAGGACAGGACAGGAGTGG

FIGURE 10

SUIITE 2

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CCCCTGGGGAGCGGAGGCGGCTGCTGGTGC GGAAGAGCTGCCCACTGCGC  
CTGCAACTCCACAACATCTACCTGGTGTATGGGGGGCAGCGGGAGGACGCG  
GGACCCTGAGGGGGCGGTGAGAAGGGGCTGTGCCCCATGTCCACATGTCCC  
TGTGTTCTCATGTTCCCATGTCCCATATCCAGTGTTCCTAACCCCATAT  
CCTTGACCTTGAGCCCATACCTGATATCCCTGACCCTGTCCCCATTCTC  
AGCCCCCAGTTCCTGCTGGGCCCCCACTCATGGTTGGAGGAGGTGCCATC  
CCCTGGACGCTGTAAGGCCACAAGGTTGCGGGGTTACTGCGCCCAACTGC  
AGGAGTTCGCGACCCGCTGAGCCAACCTGGGCTGCCAGCTGTGAGCCCT  
GGGAGCCACTGGGAGCATGTTGGGTGCAGCTGGGACCATTCTGGGGGTGA  
ACTGGTACCCTGTTGGATCAGTTGGGATCAATTGGGAATAAACTAGTGT  
TGACTGGGACCGTGTGTGACCAACTGGAAGTGTGTTGGAAGAACTGAG  
AGCTGCTGGGGTTGAGTGGGAGCAACTGGAAGTGTGTTGGAACAAACAGG  
GGACCAACTGGGATCACACTGTGGTCAGCTGGGATCACACTGGGTCAAAA  
AAGATCACAGTGGCCCAATTGGGGTCATACTGGGGTGAGCTGGGATCAGA  
ACGAGTTTAATAAACGTACAGTCGTCCGAGCCACCACAGAGTCAGCCCTC  
CAGCGGCGCAGAGCGGCGCAGCGCGCACTGGCTGCCCGCGGTAAGCGGAT  
GTGACGTCACCTCGCGGCGCGCTATTGGAACCTCCAGCAGCGCCCCGCGGA  
GCGCCCCAATGCCGCGGCCCAAACCGCGCAGCCCCCGGCGCGGGGCGCGC  
CCCCCCCCCGGCCGCCGCCGCCACCCCCCGCGCGGCTCGCGGTGAGTG  
CAGCCCGTAGGAGTGCAGGAGTGTGGGGGCGGGGGGGGGGGCGTCTGGAGC  
GGAGCCTTTATCACCGCTGTTTTCCCGATTTCCTCCCGTCTTTTCGCCCCGT  
TTCAGCCCGCCGGTACCGGCCCGGTGAGAGGGCGCTGCGGGAGATCCGCC  
GCTATCAGAGCAGCACCGCTCTGCTGCTGCGCCCGCCAGCCCTTCGCGCGC  
GTGGTAACGGGACTGCCCCGGAACGGGACACCCCCCAACCCCCCAACGG  
GACCATCCCCCACGGATGGATCCCCCCCCACACACATCCAACGTGGGAC  
CCCCCGCCCCAAAATGAGATCTCAACGTGAGATCTGGGGGCCTCAAAATG  
AGACACTCTCCCCCTCCCCCAACGGAACACCCCGAAAATGGGACCACAC  
ATAAAAGTGGGGACTCCCCCTCTCCCCCCCCGCCCCGTCAAAATGGAACAC  
CCCCAACTGGACCTTTCAAAAAATAACATTCCCCCTCCCCCAAAAATGGG  
ACTTACCACAAAGTGGGATCTTCCCCCAAAATGAACACCCCTCAAAATG  
AGACCCCTCGGACCCCCCCCCAACCCCTCTGCACCCATCNGCCGTCTGCA  
CGGAAGGGAAAGGCTGTAGGGTACATCTACCCTTATTCTTGGGTTTGTG  
TTTTGTTTTGTGTTATTTAGAAGCAAAACCAAGACAACAAAGCCAGCC  
AATGCCATTTCTGGCAGTGGACGCAGGCGCAGGCGGGTTGGTCACAAAG  
CAAGAAGTTGCTGCGGGACTTTGTCTGTTTTGGGGCCGTTCTCGTGAACCT  
CTGAGCCATGGATGAGGAAATTACTTATGCTGATTTAAGGCATCCTACGG  
GCAGTTTGCTCCTGCTAAGCGGCAGCGGTAAGGGATGCTCTGTGTGG  
TGGGTGCTCACCGCAGGCTTGGTTTGGGGGCTTGCTGTTCTCTGAGAAAC  
ACCAGCAATGCTGGTTGGGTTCTGGGTCCACCCTGGCTTGTATGGGGGAG  
TAAAGGAAGGGGTGGGGGAGAAGGAAGCCTGGGAATGGCCAGAGGTGTGG  
TGGTTTT

FIGURE 10

SUITE 3

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GTCCCTATTCCCATTGTGTCTCCTCACATCTGCCATCTCTTCTGTCCCCAT  
CTATGCTTTGTGCCCCCATCCCTTACCCCATCCCCACGTGTCCCTGTGG  
TGCCACCTCCACACGTGTCCCGTGTCCCCACAGCGGGGCGGTGGCGCAA  
TAACACTGTGATGTGGCGCTGTGCCGGGACGGAGCGACGGCGCTGCCCA  
TCCGTGCCACGTGCCAGCAGAGGGGACAGCGGGTGACGACGGCCGGGGGC  
TGCCGAGACGCCCTTCTGTCAGTGCTGTGAGGTGGCACAGAATCTGCGGCG  
GAAGGGACAGCGCGGGGGGTGGCACGGGGTGAGTGTGAGCAGTGTCCCC  
AAAGCGGGGAGGGGTGACCTGGGGTGGTGGCGGTGGGGTGTGGGGGAGTT  
GTAGAAATGGGGACCCATTGGTGTGGGGAGGTTTGGATAAGGGGTCCCC  
ATGGGTGGTGGCACATGGGGACATCCCATAGCCTGGGATCCCATGGTTGG  
GGCCATCCCGTACCTGGGATCCCCACATGGGAGGATGTCCCCCGCTGTCC  
CCATGGCAGTGATGGAGGCACAGCTGGCAGAGCAGCTGTTGGATGATGAT  
GAGGACGTCCCCACGAGGAGCTTCTTCCCTGAGAGCTGGCTGTGGCGACG  
CATCCATGTTGCTGGCACTGCACGGTGTGTCCCCGTGTGTCCCCATGTCC  
CCATGTCCCCATGACTTTGTGTCCCCGTGTCCCCATCTCCCCATCTCCCC  
AGGCTCTCAGTGCTGCTCCCTGACTCCATCACTACGTGGGAGATTCAGGC  
AGTCGCCATCGTCCCTGGACATGGTGAGTGTACCCCCCTCCAATGGCCCT  
GCAGTGTCCCCCTGACATCCCCCTCGTGGTGTCCCCATGTCCCCCACGTC  
CCCAAGTTCCCTATGGTGTCCCCATGTCCCCCTCTCCCCCTCCCCCGGA  
ATGTCCCTGTGTCCCCGTGGTGTCCCTGCACTGCCCCGAGTGATGAGGT  
CCTGGCAGGGCTGTGCGTGGCGGAGCCGACGCGGTGACGGTGACACAGG  
ACGTGCGTGTGGCGCTTTGGCTGCCCCCAGCATCCGGCCCCCTAGAGCAG  
ATGCAGCTGCAGCCCCATCCACAGCAGACTGCCCCGACGATCAACGT  
AAGCCCTATAGAGACCCCATAGGCACCCAGAGATACCTCTTTCCCTCTA  
ATAAATAACCACTTTGCTTCCAATAGATAACCCCTCTGCCCCATAGGTACC  
CCTGTGCTCCATACTTGGCCCTGCCACAGCATACATACCCCTTTCCCTCCA  
ACAGATATGCGTTGCCCCATAGATACTTCTTCTGCCCTATAGATAACC  
CCTCATGCCCCACAGATTCCCGTTTCTTTCAATTGGTACCCCTGCCCC  
TCATATATCCCCCTGTACCCACGGATACCCCTTAGACACCCGGTACCA  
CTTCTGCCCCATGGATACCCCTGTGGCACATAGATAACCGCTTCTGCCCC  
ACAGATAACCCCTTCCCTACTCCACTGTCCCACAGCCCCCACTGCCCCATG  
GCCACCCATAGCCTGGTGGCATCGGGTGACAGTGACGGTGATGCAGGTGA  
CGGTGACACTGTGCGCAGTGGAGGGGGTGTGCGCGGCGCTGGATGGGGTC  
CCCCAGATGCTGGAGCTGCCCCCGGGGAGGGCAGTGGCTGCACCCCTCAC  
TCTGGTGGCCCTCCACCCTGGGGACATCCCCATACCCATACCCGCCCCGCG  
GGGACTGGGGGCTGGGGGACCGTGTACCCGAGTCTGTCATGTGAGGTG  
AGATCAGTGGGGTCCCCTCCAGTCACTGGGTCACTCTGGGGTCCCTTA  
AAGCCCTGCGACCTCCTGGACATTGTTGTCTTGTGAGCCTGCGGTCACC  
CTGAATACTGGGGCTGTCACTTTGAGGTTTATGGACACCATGTCCCTGTG  
TCATGGTGGCCCTGGACATGTTGGTCTTATGGGATCTGGGGACATGGG  
GTCCTTGGTGGTCTGGATACTGCAGTTGTCTTTTGTGGACACTATGTC  
CCCATGTCTTGGTGGGAATGGTGTATCCATTCCCGCAGCCTGAGGGAG  
AGCTGCACCTGGAGGAGAGCACCTACATCCTGGACGAGATGGTGGGTGT  
GAGGACTGGGGGACACTGGGGAACTGGGGACGTGGGGCCGGACCCTGTG  
GTGTGGTGTCCCTACAGATAAGCGGAGCCGAGCCTGAAGCTGCCGGGGG  
ACGTCCCTGCAGAGATCGTCCCTGATGGGGACTTCAGCATGAGCATCCGT  
GTCAGTGGTGTGTGGGGATGGGGACATGGGGTGGGGACATGGGGGTGGGT  
ACTGGGAACGTGGTGGGGATGTGGTGGTGGGCATAGGGGACATGGGGACA  
TGGGAGGACATTTGTTGGGGACATTGATGTCCATCCCTGATCATCTCTCT  
GTCCCTATGTCCCCATACCCATGTGTGTGGCCATGTCCGCACGCTGTGCC  
CCTGTGTGTGTCCTGGGTGTCCCCACATGTGCTCACATCCTTATTACA  
TCCCCACATCTCCTGTGTACAACCCGCTGTGCCCTGATGTGTGCCCTCC  
ACACATCCCCATGGGTGTCCCAATGTTCCCATGTCCCTCTGCTCATCCCC  
ATCCACATCCCCATGCCATCCCTATCCCGACGTTCCCCCATTTCCCA  
TCCTATCCCCATGTCCCCTGCTCCCATGCTCCCATGCTCCCTGCTCCCA

FIGURE 10

SUIITE 4

FEUILLE DE REMPLACEMENT (REGLE 26)

TATCCCTGTCCTTCAACTCCCCTCCCATCCCCACACCATCCCCATGTCTT  
CTGTCCCCACACCATCCCCATATCCCCCTGTCCCCCTGTCCCTGTCCCA  
GGCCGGGTGCCGGGCTGGGCACTGCAGGGCGCTCTGGGGATAGGGGACTC  
TCTGCTCCGCTCCCCCGGGGCTGTGGGGAGCAGTCCCTGATGTCAATGG  
CACCCACTGCTGCTGCTCTGCGCTTCTGGATGAGAGCGAAGGGTGGGGG  
CAGCTGCCCCAGGGCACCGACAGCGCGGCCCTCAGAACCCTGCAGCAGGG  
TGAGCTATGGGGCAGGTTGTGCTTTATGGGGTGGGCAATGCTTTATGGGG  
TGTGCAGTGCTCCAAGGGATGTGCAGTGCTTCATGGGGGATGCAGTGGGG  
TTTGATTTGATTTGATTTATGGGTTTGCATTTCTCCTCCGAGGATTGCAT  
CTCTCTATGGTGTTCGAATGGGATGTGCAGTGCTCCAGGTGGAGGTGCA  
GAGCCCTATGGGGGTGCAGTGCTGTGTAGGGGATGTCTGTGGTGTCCCCA  
ATGGTCTCTGATGTCCCCACAGGCTTCGAACGGGTGCAGAGCTTCCGCAA  
AAGTGACGGCTCCTATGGGGCATGGCTGCACCGGGACAGCAGCACCTGGT  
GAGGGGAGCGGGGATGATGTGGGGACATGGGGATAGTGAGGGGATGTGGG  
GATGCTGGGGTATGGGGATGTGAGGACATCATAGGGACATGAGCGGTGGG  
GCCATGTGGATTGGGGACGTGGTGACACGGTGCTCGGTGCAGGCTGAC  
GGCACTGGTGCTGCGTGTGCTGGCCCTGTCCCGGCCCTATTGGCCAGTGG  
CTGCCAGCGGGCCCCGCTGCGTCCCTGCGGTGGGTGCTGGGGCAGCAGCGC  
CCAGATGGCGCCTTCTTGGAGCACAGGGCTGTGGTGCACCGTGAGATGCA  
GGTGGGTGACACATCACTGCTGTGTGCAATGTCCCCATGCAGGATCTCCC  
CCTGCAATGTCCCTGAAGTCCCTGCAGGCTGACCCACATTACACTGT  
GTCACTCACGTGTCCCGTGTCCCGAGGGTGGTGTGGCAGACCCCGGGCC  
GGAGGCCACCGTGTGCGTGCAGGCCCTTCGTGGTGGTGGCCCTCCATGGT  
CCCGCGCTCTGCTGCCCCCGGACAGCCCTGAGCTGCCCTCCTGGTGAGT  
CCCCATGTCCCCAACCTGTGTCTTGGTCTCATATCCATGTGTCCCTTGT  
GCCCCATCCCCAAATCCCCACATCCCCCATATGTTCCCATACCTGCTG  
TGTCCCCCAGTGTTCCCCCGTCTTTCATTCTCCACTATCCCCCGTATTC  
CCATATGTCCCCCTGTCCACAGTGTCCCTCATCCCTCTGTGTCCCCCT  
GTCCCCCAGTGTTCCCCACGTCCCTGTATGTCCCCATGTCTCCTAGTGT  
CCCCATGTCCGTGTCTCCAGTATCCCCATGCCTCCCCGTGTCTTCA  
TGCCCCACACTCCAGTCCCCACACTCCATGTCCCACTGCCACAGGACAA  
ATCCCTGTCCCGGGCCTCCAGTTCCTCCGGGGCCGCGTGGAGCAGTTGG  
GGACCTATGGGACAGCCATTACATCCTATGCATTGGCACTGGTGGACACC  
GCTCCTCCGGGGCCGATCCGGCGGTGGAACGTCTGCGGGGCATGGCCCG  
GAGCGCCCACGGTGCGTCTGTCTGTCCCCATGGGGTGGTGGCACCTCT  
GTCCCCATGGCTGCTCCTGGACCCCTCTGTCCCTCCTCAGATTCACT  
CTCATTGCAATCCTTCAATTTTATTCTCCCTCAAACCTCTTCTTTGTA  
TTCTTACATTATTCTTCAATTTTGTTCCTCCTGATTAATTCTCTTAAATTA  
CTCTCGATCAAGTTCTGCAGATTGCTTCCACTTCGGATGGATTCTTCTCC  
AAACTGTTCTTCAAGTTCATCTCCTTCAATTTCTGTCTTGTAAATTAAT  
CTTCTTCAAGTGTATTCTTCAAACCTCTTCTTCAATGTTCTTCAAGTCCA  
TTCCCTGCACTGACTCCGGGTGCTCAGGACCCCCCGTGACCCCATATGA  
CCCCATATGAACCCCCCATGACCTCCACAAAACCATATGACCCCGTGACC  
TCCCATGACCCCTCATGACCCCATATGACCCCATGACCCCATCCCTGT  
GCAGGTGGCCGTGCAACCTTCTGGCCATCCGGTGGCCCCGCGACACGGT  
GGAGGCGACGGGTACGCCCTTCTGGCACTGCTGCAGAGCCGCGACATCG  
CCGGGGCTGCGAGGGCGGCAGGTGGCTCCGACAGCAGAGCAATTACGGG  
GGTGGCTTCACTCCACGCAGGTGGGTGGGGTCACTGACCCCGGGTG  
CCTCGGGGTGGGGGTGATTTGATCCCAGGTACCTCTTTGGTGGCTGTGT  
CCCCAACCTGCTTGGTGTTCGCGCAGGACACGCTGGTGGCCCTGGAGGCG  
CTGGCCAGATGTGGCTGCACTGGGGCCGTGGGAACACAATGGGGCTGAA  
CCTGGGGCTCTCCTGGCCGGGGGTGCCCGGGGAGGGCTGGTGGCACTC  
AGGTTATGCTGAAGCCGGGGCTGGAGCCGTGGAGCAGGAGCTGCAGGTG  
GGGACATGGCGGGATCTGGGGACAGGAGGATGTGAGGACACTGGGGACA

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

SUIITE 5

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TGTCTGGACTTGGTAGGATGTAACATGAAGACACTGGGGACATGGTAGGA  
CATGGGGGACATGAGAACACGGGATGTGGGGGACATGGTAGGACATGATG  
GACACAGGGCTTTGGGGTCTTGGGTCTCGCTCTGTCCCCATGTCCCA  
GGTGCCTCTGGGCAGCCAGTGACAGTGCAGGTGGAGGGACACGCCGAAG  
GGACGCTGACGGTGGGTGGCTGCATGGACATTGGTGTCTCTCCAAGACC  
GATGTCCCTCACAACCTCCCTCATGGTGTCCCTCATGCTGCCACGGT  
GTCCCTGTCTGCCATCATGGTGTACGCTGTCCCCAGGTGCTCCGCCA  
GTTCCGCTGTGTCACTCCGAACGCCACGTGCCAGGCGCTGCACCTGG  
AGGTGGCCATCACCGGCCCCATCCTGTACCATGGTGAGGCCCCACCCAAA  
GGCCCCGCCCCCTTTCTCGCGGGGGCGTGCCCTCAACCCTGTTTTGC  
ATATCCCAACCCAGCAGATGAGGACTACGAGGACTACGAGGACTACGA  
GGAGGCGGAGCCTAAGGAGGGGAGGAGCCTACGGAAGGGGCGAGTGGCCG  
TGGAAGGGGCGGGCCAGCAGATGACCCCGCCCCCTCAGCCCCGTGTCC  
TTATGGGATGCCCGTAAGCGGCAACGCCGACACACATAACCCTGCCCA  
CGAGGTGGCCTTCTGGTCTGCTTCCGGTGAGGGGCGGAACCTTCTGTCC  
CTGGGGGCGGGTCTTCTGTCTGATGGGCGTGGCTTATTGCTGAGGGGCGT  
GGCTGTGTAGGCGGAGCCCAGGGGTGGCACTGACTGGGATGGCGGTGG  
TGGAGATCACTCTGCTCAGTGGCTTCTCACCCCATAGAGCTGACCTGGAC  
AAGGTAGGGGCGCCAGGGGACTTGTGGGACATGTTGGGGGGTTGAGGGGA  
GTTATGGGGTGTGGGGTTTGGGGTGTGGAGTTGTTGAGGTGGCAGAAT  
GTTTGGGTGGAGTCATGGGATATGGGGCTATTGGGGTTTGAGGGTGTG  
TGATGTTGGGAAACATTGAATTGGGGTTGTTGAGTTTGAGGGTGTGGGG  
TGTGCGGGTGACAGAGCTGCAGCTGCTGGGTGGAGTATTAAGGTGTTGGG  
ATGTTGGGGTGTGGATGGCTTGGATGCGGGTGTGGGGTGGGCACGTAT  
CTGGGTGCTGTCTCCACAACAGCTGCGGGACGTGGTGGATCACTGGAT  
CAGTCACTATGAGTTGGAAGGAAACAGTTGGTGTCTATACCTGGATGAGG  
TGTGTCTCTCCGTGTCACCCTATAACCCAGTGGCCCCATGTTCTCATAT  
CCCCCATGTCCCCGTGTCCCCACACCATATCCCATCTCCCCACACATCC  
CGGTGTTCCACCACGTGTCTCATTTCTGTCCCTGTCCCCAGGTCCCCC  
CGAGCGGCAGTGTCTCAGTTTGGGGCCACCCAGGACGCGGCTGTGGGT  
ACATGCAGCCGGCAATGGCAGCCATCTATGACTACTATGAGCCTGGTGGG  
TGGGGCCTTCAGTGGGAGGGGCTAAATGGGTGGTGGTCTTCATGGGTGT  
GACCATGGAGGAGGCGTGGCCGATCTGACCCCTCCATGCCCATCCAGG  
ACAGCGCTGCACCGTCTTCTACAACGCCCCCAAAGGAGCAGCACCATCG  
CCACACTGTGCTCCCCAAAATCTGTGAATGCGCCCAAGGTAGGACCCCA  
CTGTGACTCCATATGTAGGGCCCCCATCCAGTGAACCCCAACATCTCTCT  
CCTAATTTTTGAAGATCTGGGGGTGAAATTATGGGGTTTATAGGGGAGCG  
TGTTTGAAGTGCATGCAGGACATGGAGGGAACCCACACCAAGAACCTTGT  
GTTTTGGGTCCCTGATGATGTTGGGAGATCCTATTGATGTTGGTGGTCCC  
CAGGGGGGTGTCCCCAAGCCAAAGGAGGACACAGGAGGTGACAGCTGAT  
GACCGCATGACTTTGCCTGTACAGCCCCGCGTGGACTATGGTGAGAT  
CCCAAATCACTGCACCTCAAACCTGACCCCAAATTGGCTGCATCCCGAAC  
CCCAACTGCCCTAAATCCCATCTGCTGCCCCCTGAGTCCCACAGCTGCACA  
CTGTACCCCAACAAGTGGCCCCCTGAAGCCTAAAAACATTACAGGATTTT  
GTAGTTTTCTCCCTGTACCCCAAGTTGTCCCTCTGACCCCAAGAACCCAC  
AGCTGCCCTATGCTGTCCCCTGCCCCGACATACTCTCTGATACAATAAC  
CCCCGTGACCCCATCTTTATGACCTCCATGACCTTTGACCCCAAGCACTG  
GTGGTTCGGGTGCTGTCCAGAGTGAGATAGGGGCTTTTGTGGCGTTTGA  
GACGGAAATCAAGGAGGTGCTTGAAGGTGAGACTGAGGGTAGTGGGA  
CGGACTGGAAGGTGAGAATGGGAGCACTGGGAGAGGCAGGGAGTACTGAG  
AGGGACTGGAATGACTGGAATTTGAGACTGGGTGGACTGGGAACCTCTGG  
TAGAGACTGAATGGGTATACTGGGAACACTGGAAGAAGTTGTGGGATGAG  
AAGAGGATGCTGGGATAGGAGACCCCCCTTGTGTCTAGGGGGGTCTCT  
CAGCCATACTGGCACAATATGAGAGTATACTGGGTGGTACTGGGAAAGCT  
GGGAGGACTCATACTGGT

FIGURE 10

SUITE 6



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A5FINB.txt

CCCCCTGGGGAGCGGAGGCGGCTGCTGGTGCGGAAGAGCTGCCCACTGCGC  
CTGCAACTCCACAACATCTACCTGGTGATGGGGGGCAGCGGGAGGACGCG  
GGACCCTGAGGGGCGGTGAGAAGGGGCTGTGCCCCATGTCCACATGTCCC  
TGTGTTCTCATGTTCCCATGTCCCATATCCCAGTGTTCCTAACCCCATAT  
CCTTGACCTTGAGCCCATACCCTGATATCCCTGACCCTGTCCCCATTCTC  
AGCCCCAGTTTCCTGCTGGGCCCCCACTCATGGTTGGAGGAGGTGCCATC  
CCCTGGACGCTGTAAGGCCACAAGGTTGCGGGGTTACTGCGCCCAACTGC  
AGGAGTTCCGACCCCGCTGAGCCAAGTGGGCTGCCAGCTGTGAGCCCT  
GGGAGCCACTGGGAGCATGTTGGGTGCAGCTGGGACCATTCTGGGGGTGA  
ACTGGTACCCTGTTGGATCAGTTGGGATCAATTGGGAATAAACTAGTGT  
TGACTGGGACCGTGTGTGACCAACTGGAAGTGTGTTGGAAGAACTGAG  
AGCTGCTGGGGTTGAGTGGGAGCAACTGGAAGTGTGTTGGAACAAACAGG  
GGACCAACTGGGATCACACTGTGGTCAGCTGGGATCACACTGGGTCAAAA  
AAGATCACAGTGGCCCAATTGGGGTCATACTGGGGTGAGCTGGGATCAGA  
ACGAGTTTAATAAACGTACAGTCGTCCGAGCCACCACAGAGTCAGCCCTC  
CAGCGGCGCAGAGCGGCGCAGCGCGCACTGGCTGCCCGCGGTAAGCGGAT  
GTGACGTCACCTTCGCGGCGCGCTATTGCAACTCCAGCAGCGCCCCGCGGA  
GCGCCCCAATGCCGCGGCCCAAACCGCGCAGCCCCCGCGCGCGGGCGCGC  
CCCCCCCCGCGCGCCCCCCCCCGCCACCCCCCGCGCGGCTCGCGGTGAGTG  
CAGCCCGTAGGAGTGCAGTGTGGGGGCGGGGGGGGGGGCGTCTGGAGC  
GGAGCCTTTATCACCCTGTGTTTCCCGATTTCCTCCCTTTTCGCCCCGT  
TTCAGCCCCGCGGTACCGGCCCCGTGAGAGGCGCTGCGGGAGATCCGCC  
GCTATCAGAGCAGCACCGCTCTGCTGCTGCGCCGCCAGCCCTTCGCGCGC  
GTGGTAACGGGACTGCCCCGGAACGGGACACCCCCCAACCCCCCAACGG  
GACCATCCCCCACGGATGGATCCCCCCCCACACACATCCAACGTGGGAC  
CCCCGCCCCCAAAATGAGATCTCAACGTGAGATCTGGGGGCTCAAAATG  
AGACACTCTCCCCCTCCCCCAACGGAACACCCGAAAATGGGACCACAC  
ATAAAAGTGGGGACTCCCCCTCCTCCCCCGCGCCGTCAAAATGGAACAC  
CCCCAACTGGACCTTTCAAAAAATAACATTCCCCTCCCCCAAAAATGGG  
ACTTACCACAAAGTGGGATCTTCCCCCAAAATGAACACCCCTCAAAATG  
AGACCCCTCGGACCCCCCCCCAACCCTCTGCACCCATCNGCCGTCTGTGCA  
CGGAAGGGAAAGGCTGTAGGGTACATCTACCCTTATTTCTTGGGTTTGTG  
TTTGTGTTTGTGTTATTTAGAAGCAAAACCAAGACAACAAAGCCCAGCC  
AATGCCATTTCTGGCAGTGGACGCGAGGCGCAGGCGGGTTGGTCACAAAG  
CAAGAAGTTGCTGCGGGACTTTGTGCTTTTGGGGCGGTTCTCGTGAACCT  
CTGAGCCATGGATGAGGAAATTACTTATGCTGATTAAAGGCATCCTACGG  
GCAGTTTGCTCCTGCTAAGCGGCAGCGCGGTAAGGGATGCTCTGTGTGG  
TGGGTGCTCACCAGGCTTGGTTTGGGGGCTTGTGTTCTCTGAGAAAC  
ACCAGCAATGCTGGTTGGGTTCTGGGTCCACCTGGCTTGTATGGGGGAG  
TAAAGGAAGGGGTGGGGGAGAAGGAAGCCTGGGAATGGCCAGAGGTGTGG  
TGGTTTT

FIGURE 10

SUITE 7

45/110

Conti131.txt

AGAAGAGCCCCGTGATGTCCTCCAGGTGCGGTCCCTCGGTGCCTGTGGGG  
ACAACGACAGCCCTAAGCACAGTGTACCATCCTGGGTGGGGTCCCCAAC  
CCAAATCCATGATCTCCCATTTGTCCAGGCCATGGTCTGATGTCCCTCA  
GACCCTCCTAACCATGGTCCCAGCATCCAATACTCCACGTGTTTCCAA  
TATCCCCACATCCCCCTCACCAGCCAGGAGCAGTCGGACGGAGACACGC  
ATTGGTTTGGCCAGTGCAGTGTGGGTGACAACGCAGCTGTAGATGTCCCC  
GTGGTGTGGGGGCGTGCGGGGATCAGCCGTGCTGCCGCCGTCCGGCTGT  
AGGTTCCATCGGCTGCCTGGCGGTGACCTGAAGTCCAGCTGTCCATCACT  
GTGTCCCTGGGTGACTGTGATGTCCCCGAGCCCCCGGCGGGCGCTGCCA  
CGTCACCGTCACATCCAAGGGGTAGAAGCCAGACACGTGGCAGCGTAGCT  
CTGCTGACGTCCCCGGGGGCCACCACCAGGTTCTTCGGGGACAGCGTCACC  
TTGGGGGGCTCTGGGAGACATGTGGGGGGACATCGGTCCCATATAGCCCA  
TAGGGCCCCCTCCTATAGGGCTCATCCCCCCTATAAACCTACAGGTGAAC  
TATGGGATGATGCCACCCCATCCTATAGTCTCATAGGAATACCACCCGG  
TCCCATCCACCCTATAGCCTCCATAGGAATACCACCCAGTCCCATCCACC  
CTACAGCCCCCACAGGAATATCACCCAGTCCCATCCACCCTACAGCCCC  
CATAGGAATACCGCTGCTCCCATATGTCCTATCTGACCAATAGGAATAC  
CACCCAGTCATACACACTCCGTAGGAACACTGCCAACCCACACCCCAT  
AGGAACACCGCCTGCCCCACATGGACGCACCAAAGACGTGGAGCTGCAGC  
ACTGTCTGTGTGTGCCCGTGGGGCAGGAACACGGAGCAGATGTAGGTGCC  
CTCATCCCCCGGTGATGGCCGCCAGCCGCAGTGTACCCGCTGTCACCC  
CGTCCCCATCCCGTGTCCCCAGCAGCAGTTTCGGCCCCGGGGGTGGCGCGG  
GGGGCGCGGGCGGTGGAACGTGCATAGG

FIGURE 10

SUITE 8

46/110

AB1B3FOR.txt

CCAACTTCCTTTGGTTCAGGGAAGAAGACTCACCCACTGCTTTGGTTTGT  
 TGCCTGGAAAAGCATGAAGAAAGCACCACATGATGAGAGGAACAGTTCA  
 TCCCACAGCTCACGCAGGAAGAACCATTTTTAAATTTAATTGGGAGGGA  
 GCACTCACCCAGGTCTGAAGCTAGTTTATCTGCAATGAAACAAATAAGAA  
 ATGCATGATGAGAAGGGTCAGAATATCATCCCATGGCTGATCCCATGGGA  
 AGACCCCGAATCTCTTTGGTTTGCGGAGGAGGACTCACCCAACGTGTCAT  
 TCCTTCCCTCTGCAAAGGGAAAGCAGAAACAGTG

FIGURE 10

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SUITE 9

47/110

AB1C1FOR.txt

TGGGATCAAGTTGAGTAGACATAGCATCCTCGCTTTTAGACAAGACCTGC  
ACAGTATACCACCGTTTACTGTGCAGATAATGACCAAAAGCAATATGCGT  
CACACTTTTCTGGTGACAACGTACAAAATGGCGGTCGTCAATCTGCCAGACCTGG  
AACAGCACAAACGCCCTTTCTCATCGAAGATTTCAATCTGCCAGACCTGG  
TGACGCGAACCAGAGATGCAACGGTTTGCATACGCCGCGCACCCGCCCTTC  
TCGTGCCGAGCGGACGTGGTTAGCATTGATTTCCAGACCAACCACTTTT  
GCTCACCTTCGGTACATAAATAACCGGCAACGGAACCGATACTTTCCGGCC  
ATTACCACGGGTGCTCCTCCATGCAGCAACCCGAAAGGCTGCTTTGTCCG  
CGAGTCTACTGGCATTTGTCGCTTCAAGGGTGTTCATCACCAATATGTTCAA  
AGCGAATATCCAGGAACCCCAACCATGTTTCCTTCAACCATAGCATTCACT  
GCTTCCAGGGTGATTTTCCGTTTCCAGATCATTTAATAATCTCCAGTTAA  
AGCCTGCACAGGATGGCTTACCCCGTGCCTTCAACCCGTTTTATCTGGCT  
ACGGCAAGGAATATCCGTT

FIGURE 10

SUIITE 10

48/110

AB3A11RE.txt

CCGTCGCCTCGGCTCTCCCTCGGGCTCCACCCCCCGTTCCGCCCTTTG  
 CCGCCGCATCTCCCGCTCTGTACCTCCCCAAGAAGTCGCTCAGACGGCG  
 TCGCGTTGTCTGCACATCCTCGGGGACCGTCTGTTGTGCGGCAGCAGGGG  
 AGGGGAGCGGGCGGTCTGTGCTCTTCTATTCCCTTCAGTACAAGAAGGTG  
 GTTTGGGTTCTTTAACCAAATATACTCTTTTGTFTTTGCATAAAATCACC  
 AGAAGGAATTGGTCTGTTGAATATATAGGAGTGGTGGAGAGAGTCGAAGA  
 AGTGTTCCTGTGACAAAACACCGTTAAAAGTGAATTCATGGAGAACGCA  
 CTGCAGTGACACAGAAGGGAAAACACGAAACATAAATAATTGCCGATTT  
 ATCATCGATTTAGGGTCCTTTGGGCTGATTGCTTTCCCAGTATTCCCT  
 TTGGAGAAAACCGGTGAAAAATGG

FIGURE 10

SUITE 11

49/110

AB5B6FOR.txt

TCACCTGGCTTTGCTGCTCCAGACCCCGCAGGAAGCGACCCCCCTGGCCC  
CTGGCATCCCGCAGCCCCACACGCAGCTGTGCACGGCCCCACACTGGCGC  
CCCATCTGGGAATCTGGGGGTCCAAAGGGTCAGTGGAGTCAGGCGGGTCC  
AAAGGTCAGTGCAGTTCAGGAGGTCCCCAGATGTCAATAGGGTCAGGGGGA  
GGGATCCCAAAGGCCAATAAGGTCAAGGGGAGAGATTCCAAAGGTCAGTA  
GGGTCAAGGTGCCCCAGAGGTCAATAGGGTTGGGGGAACCCAAAGATTAT  
AGGGTCAAGGAGTGACCCCAAAGGACATCAGGGCCACTGATTTGGGGTGG  
ATGGGAGAGGAATTTGGGGAGTTCAGGAGAGTTGGAGGGGATTTGGGAGG  
TTTTGGAGGAGACAGATGGGGATTTTGGTGGGAATTTGGGGAAGATTGGG  
TGGGATTTGGGATTTGGGTGGGATTTAGGTGGGGATTTGGGGGGATTTTG  
TCTCTGGGTGTCCCATAC

FIGURE 10

SUITE 12

WO 99/27132

PCT/FR98/02501

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AB6E4FOR.txt

CCTGAAACTTTGGGGTGAGCATCTCCATCAGCTCATCTGCAATGCAATGG  
GATCTTCCAGTCTTTGGGTTTTGTGCTCGTTGTGCCACTATTTTCATGGC  
ATCCTAAGATGGTGTGTATTATTTTTGTGACACTGTAAGAGACTGGAGC  
AGAAATTTTGTACAAATTAACAAAAAAAAAAAAAAAAAAAAA

FIGURE 10

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SUITE 13

51/110

AB6G8REV.txt

GTTCTATGATTTCTTTGGTCCGAATACCATGAAATCTGATATTTCCATTT  
CAGTATCTGAACTGGGTTCTCTGCTGGATCACAGTGGTCCACACAAAGAA  
GCAGAACAGTATATCGCTCGCGTCTTTAACGCAGACCGCAGCTACATGGT  
GACCAACGGTACTTCCACTGCGAACAAAATTGTTGGTATGTACTCTGCTC  
CAGCAGGCAGCACCATTCTGATTGACCGTAACTGCCACAAATCGCTGACC  
CACCTGATGATGATGAGCGATGTTACGCCAATCTATTTCCGCCCGACCCG  
TAACGCTTACGGTATTCTTGGTGGTATCCCACAGAGTGAATTCCAGCACG  
CTACCATTGCTAAGCGCGTGAAAGAAACACCAAACGCAACCTGGCCGGTA  
CATGCTGTAATTACCAACTCTACCTATGATGGTCTGCTGTACAACACCGA  
CTTCATCAAGAAAACACTGGATGTGAAATCCATCCACTTTGACTCCGCGT  
GGGTGCCTTACACCAACTTCTCACCATTACGAAGGTAAATGCGGTATG  
AGCGGTGGCCGTGTAGAAGGGAAGTGATTTACGAAACCCAGTCCACTCA  
CAAAGTGTGGCGGCGTTCTCTCAGGCTTCCATGATCCACGTTTAAGGTG  
ACGTTAAACGAAAGAAACCTTTAACGAAAGCCTACATGATGCACAACAAC  
AACTTCTCCG

FIGURE 10

SUITE 14



SUITE 15

53/110  
B5FOR.txt

ATTTGTTGTTTCAGCAGAATGCATCTGTGTGCCCCATCCCCACTCCACTTC  
ATTTCCCTTTCTTTTCCTGCAATAGGAAATCCATCTTGAGGGGACGGGGA  
CACAGGCAGGCTCACAGAGGGGACCCTGGGGTAGCAGTGCCGGATTGTTGGG  
CTGAGGCCCATAGCAGTGACCACAGAATCGGTCAATTTGTCCGTTTCATGGT  
GAAGATGGGAGGGGTTTCAGCAGAAGCACTCCCTGGGACTCCCAGAGGGC  
TGTCTCAGAACCCTGCTTTCTTGCACAGAAGATGAACCATTTTGTAG  
GGGGAGGGTCCAGGATGTGGTTGCAGTGTGAACAAAGCCTGTGTGCTTTT  
ATAATTCTCTTCTGCTGCTGCTGCTCATTCTGAGGGCTGAATGGGCAG  
CACGGGCAGACAGCAGCGTGGCTCCGACACTTCTATGTCTGCAGTGCCCA  
TTGCAGGAAGAGAAAAGAAATGGAGTGGGGATGGGGCAAACAGATGCATT  
CTGCTGAACAACAAATCCGGTATTTTTTTATTGAGAGAAATAACACAGGA  
TTGTGAGCTGATTGCATGAGCGCATGCAGCGATGTCCCCCGTGTGCCCG  
GGCAGTGTGGGGTCTGCACAGCCCCAACTCCTCACAGAGCCGTATTGCA  
GAGCTTCACCCCAACGCTGGGGCTTTTGGGGTGGGCACACATCAGAGGG  
AGGGACTGCGTTGCCCTCCATCTCCTGCACATTATGGATGGAGACGTAAA  
GGTCTTTCTGGCAGACCCACTGGTGTTCACCACTACAGACGTGCCCCC  
CACTTTTGTGTTCTTGAAGGTCCCGCAGCGATTCTCCATCACGGAAGGT  
TATCAGACCTGCAAAATAAGGCTGTTTGCACCCAAACACCCGACTTGAAG  
GAGGCGGGCAATGGTTGCAGAAATACTCACTCTGTGCTGTGTAGGAGGA  
GTTGTCCACCCATTTCATTGATTTGTGGACACTTCTAATCCAATCCACA  
CCGGCTCCCGCACTGCCATCTGCTGGAGGTGATCCTGGGAAATGGCACC  
AAATCCTTCTGCAAGGGGCTGGAGGGGTGCAGAGCCACCAAGTCTGCCTT  
GTTGGACCCCCAGCAGATGGGACTCAGACAGCAGCCATGCCTGGAATGCT  
GCCTGGCTCTGCAGGCGGCTCAATGGGTGGGAATGGCTTCAAACCCGAGA  
TGGAGGCACCGGTGTGACCAGCTGAGCTCTGCTTCCATCCTTCAGCCTGT  
TTGAAGGGTGGGAGGGGACACAACCCCATGTCCCACCCCTAGCCTGAAC  
CTTGATGTCCTTAACCTCAAACCATATGTGCGCAACCCAGCGTGCCTGA  
CCCCAACCCGTGTGCCCTACTGCCATGTGTTGACCCCTAACCCCTAAAGGGC  
ATAATCCAGACCCCAATCTCTCCAGTGATGCTTTAGCCCCATTGGGTTT  
GGAACCACTGACCCTCCTGCTGCCGCCAGTCACTCCAGAGCGGTTTTCT  
CCCACAGAATCCACCAACCCACACATTTTTCAGGTCCCGTCCAGCTCCCT  
GCTCTATGCTTACCTCTTCTGCCTTCTTCCGGAGCACAGCCAGCTGAGAC  
TGCAGATTTTACACTTTCATTTTGTGTTGTCCAGTTCCCCTTTTCTGT  
GGAAAGCTCATAGCATCGGTCCCCTAAAAGCCTCCAGAACTGGGGACAGA  
GCAGGCAGGCAGGGGCTGGAGAGAAAGAGCCGTGAGCATCTTCAGGT  
GGGAGAAATCCCACCCAGGAGGATTTCCTTGGGAAGGGCATTACCTGCAG  
AGCTGTTCCATGTGGATTGGCAGAACTGCTCAATGGAGGTATTCTCG  
CAGAGCTCTGTCCCATTCCTCCCGTTGGTCTCAGGGCAGTGCCGGGCAGC  
GCTTGGAGGTGGTGTGTTTTCTGAAAGACTTTTGGGCACAACCTGGGGT  
GAGACGCGGCCCTATGGGGCCAACCCGTGGAACACGAGGGTGGGG  
TTGGATCCTCGAGCTCTTTTGCAAAGCCTTTCTGGCTATGGTTGCACTCA  
GTTAATTAACTGTCTAAAACCATATTTTGTATATAATTAGACATGATGT  
TTACTGCTTCTGCTCCCCCTTGGTTTAAAGAGCAGAGAGGCTCTTGCAGA  
AGGGAATTCTCTCACTGAGTGCCACTTTGGAATTGTTGTGTGATCACC  
AACTCCAGTGCAAAGCCCCAGCCCCACTTTGGGCAGAATGAATGTGTTT  
TCTGCTCAGAAGAGCTTCGATTTCTGTGCAGCAATGTGGTTGGGATCTG  
ATCACTCACCGCACAGCTGAGCCCTGTCAACAGCAGCAGCAGCAGCAGC  
AGCAGCACCCCCAGCATGCAGGCTTCTGGAAGTCCACGGAAGTGAAG  
AGCCACACTTATATAAAACAGACATTTTGAAAAAATTTTCTTTTACA  
GAAATGATCTCCCTGTGAAAGAGCCCCCTCCACCAACCTGCTACGTTAGAG  
CAGAAGTTGATGGCTGCTTTGGTTTCTTGGAGATTGGGGTCCCGGACC  
CTTCCCATTGGTCCCATGCTGTGATGAGCAGAAGTTGATGCCCTGTTTG  
TTTTCTCCAGTTCGGGGTCCCCCTGGACCTTCCAGTGGCTCCAGTG  
GTTCCCAGCTGGGAAGGAGGTGGCAGAGGGGTGACAGCAGCAGGGAGC  
ATGGGATGGGCTCCCGTCCAGTCAATGCAAGGCAATCACTTC

FIGURE 10

SUITE 16

WO 99/27132

PCT/FR98/02501

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B5FOR.txt

ACGCGTGGTTCTGGAGGTGGTGGAGGCCCTGCAGGCTCCATAGAGCATGG  
GGTGGGAAGCTGAGCAGCCCCAGGCTTTGTGAGCCGAGCCAGTGTGGGG  
CAGCCGGTGGCTGGGAGGGCGGGGATGTCTGCAGCC

FIGURE 10

SUITE 17

55/110

B5REV.txt

CCCAGAACCCCAACCAGCATTGCTGGTGTCTCTCAGAGAACAGCAAGCCCC  
CAAACCAAGCCTGCGGTGAGCACCCACCACACAGAGCATCCCTTACCGCG  
CTGCCGCTTAGCAGGAGGCAAACCTGCCCGTAGGATGCCTTAAATCAGCAT  
AAGTAATTTCTCATCCATGGCTCAGAAGTTCACGAGAACGGCCCCAAAA  
CGACAAAGTCCCGCAGCAACTTCTTGCTTTGTGACCAACCCGCTGCGCC  
TGCGTCCACTGCCAGGAAATGGCATTGGCTGGGCTTTGTTGTCTTGGTTT  
TGCTTTTAAATAACAACAAAACAAAACAAACCCCAAGAAATAAGGGTAG  
ATGTACCCTACAGCCTTTCCCTTCCGTGCGCAACGGCCGATGTCTCATT  
TGCTGCTCTCTGAGGGATGGAACGCCGCTGGGTTCAGCGATGGCAGTGA  
GCGACGCGGTGCTGAGCTGGGGGGTAAGCAGTGAGAAGCTGAAAAATCGC  
TGATAATAAAAGCCTAAAAATACCCAGAACAACAACAACAACAAAAA  
GACCCCAATCGAGACCTTTTAGGGGTGAGAGAGCATTGGCTGATAAGCG  
GGGATGGGGGAAGAAAGGCAATATTTGGTGATTCTGTGCCAACCGATGCC  
TCGGCAGCTGGAATACTGGGAGGGGATGGGTTTACTTTAATTACGGCT  
GTCTATTAGTAAGGCATTTAATTTATTTGCAGTCCCTTCTCTTCATGC  
TGGGTGCTGAGACGGCCGCTGCGCTTCTGTGTGCTAAAAAAGGTGTGAA  
AGGGCCCCGTGAGGGCTCTGCCTCATCCTGACCAGAGCAGGCAAAGAAAA  
AAGTGCAAAGAGCACAAAGAGAAAAGACGTTAACCAACAGAACTGCGTCC  
AGACAGCGAGAAGCCCTTCTCCTTTATGTATCTTCATTACCAGAATTGCT  
TTTTCCCCCTTTTCTGGGATAGTTTCATTGCTGCATCATCTGCTTCATTT  
CCAATTTCCCCTCCTTAACCTGCCCCATGGAAACATCTTCCGGGGGACAGAT  
TCATTGCTCCCCAGACTTTTCGACACCTCTTCCTTTGCATATTGCTGGTTG  
TGCCCATCCCTTTGCAAACCCATTCCCTTGCCAACGGAGGAGAGGATGGAG  
ATGTGTGTGGTTCTGTACGGGGTCTGCAGGAATAAGGGCTGCAAAAGACA  
TCTCAGCAGCTGCTTTGAGGCAGGCAGGATGCACTGATTCTTAGGGAGG  
GAGAGGTTATCTGTGCGGGGATGCAGAGTTTGGGCTGACCTGGAAGATCA  
GCCCTGTGCAAAATGTGGGTGAGCAGCAGAAAAAAGAAAAAATTC  
CAAAGAGTGATTTCCAGCAGGGAAAGGAGGGGAAGCTGCTTCTGGTG  
CTGGCAGCAAACTGCTGTGTCTCCATGGGAACCTCTGCTGGTGGGCATC  
TCCCCTCACCCCTTCTCATCTGCCCTGCAGCATCCACGTGGAAATCCCC  
CCTGAAAAAGCCCATTTTGTGACCATGCATCACATTTATTTTCGCATTCA  
GCATCAGACGGGACAGGCAATGGGTTGGGGGATGGGGGGGGGTCTGAG  
GGTATATCTTTTTGCTGAGCCAGGTTTTGAGTCATGGGGGATAATTTTAT  
TCCAAGGGGAGGGGGGCATTTAACTGCAGGTGGTAACAATGAAAGGCAGT  
GGGAGTTGTTGTGATTGCATGGGGGAAAGCACTGGTTTTTTCCATAAATT  
GGGACTGATGTGGCTGTTGTTGCTTATTTTTATGGGGGAGGTTGTGGGG  
TTTTTTTCCCCTATATTACATTGCATTTAATTTTCACTCCTCTCTCATTGT  
CTATCCCTGGCAATGCTAGGACTTCTCCTTGCTGTTTTCTGTTGGGCGAT  
CATTGCCACAGAGGGAGGAATTGCTTTTCAATTGGGTCACTGCAATGAGT  
TTTAGCACCCAGAAATATATCCTTATGGGTCTCTGCTTTTGGGGCACTGC  
TGATGGGTGGAAGTTTTGGTTTTGCAGGTGAAGTGGAAGCCCCAAATGGA  
GGAAGTGAGGGAATATCCCCATGTTTGGGACAGAAATGGAGCAGGAGGG  
AAGGTAACAGCCGAGCCATGCCCTTAACACATCTGTTTATTGTTATTATT  
ATTGTTATTATTTTATTGATTACTTCTTAACTTGAGAACAAGGGGAGG  
GATGTGGGTGGGAAGAAATGAGTCTCATTCTTTTAGCACTTCCCTCAA  
GGGGAATTTGTGTTGGTTGTTGAGCAGCAGGTGGACTTCTTGCTGTGA  
GCAGCCACATTTTGAAGAGTTCTGTTGTTATTAGCATTATTTATGCGAT  
TCTGTGATGTTTTTATTATAATTGTAATGAATCCTCCCTGAGGCAC  
TGGATGGGGGAAAAAACAACATTTTGGGGTCTACTGCTCACACCTGG  
GGTGCATGTTGCCCATTTGAGGTCCCTTCTCCCATAGGTCCCAGCCGTG  
GGGCATGCGTTACCTTCCAGCTCACGATGGCAGCGGTGTTACAGTGCTG  
CTCATCACTGCTGTTGCCCTTTCAGGTGAGTGCTGAGGGTTCCAAAGAGC  
AGAGAAAACCCCTTTGGG

FIGURE 10

SUITE 18

56/110

A52FOR.txt

TTCTCCACAGAATCCACCAAACCCACACATTTTCAGGTCCCGTCCAGCT  
CCCTGCTCTATGCTTACCTCTTCTGCCTTCTTCCGGAGCACAGCCAGCTG  
AGACTGCAGATTTTACACTTCATTTTGTGTTGTGTCAGTTCCCTTTT  
CTGTGGAAAGCTCATAGCATCGGTCCCCTAAAAGCCTCCAGAAGTGGGGA  
CAGAGCAGGCAGGCAGCAGGGGCTGGAGAGAAAGAGCCGTGAGCATCTTC  
AGGTGGGAGAAATCCACCCAGGAGGATTTCTTGGGAAGGGCATTACCT  
GCAGAGCTGTTCCATGTGGATTGGCAGAAGTACTGCTCAATGGAGGTATT  
CTCGCAGAGCTCTGTCCCATTCTCCCGTTGGTCTCAGGGCAGTGCCGGG  
CAGCGCTTGGAGGTGGTGTGTTTCTGAAAGACTTTTGGGCACAACCTG  
GGGTGAGACGCGGCCCTATGGGGCCAACCCCGTGGAACCACGCAGGGTT  
GGGGTTGGATCCTCGAGCTCTTTTGCAAAGCCTTTCTGGCTATGGTTGCA  
CTCAGTTAATTAAACTGTCTAAAACCATATTTTGTATATAATTAGACATG  
ATGTTTACTGCTTCTGTCCCCCCTTGGTTTAAAGAGCAGAGAGGCTCTTG  
CAGAAGGGAATTCTCTCACTGAGTGCCACTTTGGAATTGTTGTGTGATC  
ACCCAAACTCCAGTGCAAAGCCCCAGCCCCACTTTGGGCAGAATGAATGT  
GTTTTCTGCTCAGAAGAGCTTCGATTTCTGTGCA

FIGURE 10

SUITE 19

57/110

H82FOR.txt

CTGCGCTGGGGATCTTGTTCCTCCCTGGCAATGGGAACAGCTGTTGGGTG  
CCTTTTTTGGGAAAGATCTCTTTATCGGTGCATGAAGAATGAAGCGACTA  
ATGGGGAATGGAAGGAGTGGTGGCTGTTTGAGTAATTGACTGATAGGTTG  
ATGGAGGGATACTTGAATTAAGAGCTTTTGGCTCTTATCTCATTGCCTCT  
GTGCACCAGGTTTGGAGTGGGCCAGGCCCTGGCACGGTCAACTTGCTCAC  
TGTTGGCAATAGGAACATTTTTTGGCCCTCAGAGAGATTTTGTGGAGGA  
ATGGATGGATCATTATGTCCTGGTTTGTCTGGGGGGGACCAATGTGATG  
GATTAATTTTTTTCAGTATAAAAATAGTTTGTGAGGTGAACCTTCTGGTGA  
CTGAGTGGATGGTTGGATGGAGGGATGTGAGTTTCTGTGGAGGGATGGAT  
GGTTGGAAGGTTTGTGGATGCACTGTTGAGTGTGGTGGGATCTACATT  
TGGGGCAATGGATGGATGGACTCTGAGAATATAGACTATAGCTGAGTTGG  
CAATGACCAAGAAGGACCATTGCGTTTTGTTTCTGGCTTCATGTAGGATC  
ACCCAGGAATTAAACCCCTATGTCATGGTTTTGTAACCTCGCTATTGGTAT  
TCCACATCATAACATCATGGACAAAAGAGAAGAATAGCAAAGTTACAAAA  
CCATGACACCCCTACTTCTGAAAGCAGTTTTGAAATGCTTGGGGAGCTGAA  
TGGTTGATGGTGGTGGAGTCGTGGGGGGGAGGTGTCCCTGTGGGGCAG  
TCCCTGGGAAGCTATAGCTATAAGTCACCCCAATGCCCCCTCTGTGTGGG  
AGTAGTGTGGGTGGGGGTCACCTGGGATACCACAGTGGGGTGGAGCCCAGG  
GGAGTGTCTTTGAGGTCAGTGGGGGGTGAGCAGGGCTCTCTAGAGGCCTT  
TGGGGGGTCCAAAAGGAGTTGATGAGAGAGAGAGTGTGGGAGATCCATGG  
GGGGGCTGCAGGCCTCAGTGCCCTCCATCTCTTGCCAGGTGCCCCAGGAA  
CACTATGGGTGGGGACACTGTGGCCCCGAGTGCTCACCTGCATTGGGCA  
CCTCCCATGTTCCCCCTGAAGGCTACAACCTCATCTATGGACCCCCCGG  
TGGCCCCGTGAAGGTAATACCCCATAGCACTCCCTGAACCTTCCCAGGGGA  
TCTCCCTGGGTATCTCCTGGGGTACCCCAACCCTCCTTGGGGACCCTGCT  
CCCACCCTGGGGAATCCAAAAGTCCTCCACCACCCAAGCACCTAAGAAC  
CCCCTGCACCCCACTATCCCTTGAGGTCCCAATACTCCTTTTACAGCA  
TTCCCATCCTCCTCCTTGGCCCCCTTTATGCTCTCCAGAGACATTAAACAC  
CCCTGTAATGCCCTTAGGGACCCCTGCAGCAGCCCAATAATCCTCCCAT  
GTCTACCTCAGACACTGCAGCTGCCCCCTGAAGCAACATCCAAGGAGCT  
GTGGGGCCTGGAGGCCAGTGGACGCTATAGGCTGCAGCTCTGGGGCCGGG  
GGCTGGAGCCCTTGAGACCACCTTTGACACCCGTGAGCTGGGAAAGGGG  
GTCCTGTGGGTGGGAAGGGGCACCTTGGGTGGAGGACTCTGGGATACCCA  
AATACCTGGATGATTTGGGGTGTGGGGACATATGGATGCTGGGTCTGA  
AGTATGGAGGGGGGTACCAAGGAATCTGCATCCTTGGGTGGGGAGCTCTG  
GGGGTCCCAAGTACCTGAATAATGGGTACCTAGTTAGGGGAATGCCTTG  
GGGTGGGGGGGGGGGCGGACACAGCGGGATGCCCTCGTCCCTTGGTAGGTG  
AACAGGGACACCCAACCTGGTTGGGGCCACCTACACTGCTCTGTCCTTCAG  
CACCCCTCCCCACCCACATCCCCGGGACTGCGCTGAGGAGCAGCTCAAT  
GGACCGGGGCCTTCACGAGAGGTCTCATCTTCTCGGGGGCGACCGGCA  
GCGGCCACTGCACGTCTTCTGCGACATGGAGAGCAATGGGGCGGCTGGC  
TGGTGGGGAACGGGGCGGTGGGGAGGGTGTCTGGTGGGCTCTAGGGGGT  
GCTATGAGGAGTCTGGTGGGCAATGGGGGTACAGGGTGGGGTGGCTGAC  
TCCATGGTTGCCATTATAAGGGTTGGATTGGCAATAAGAGACCTGTGGAG  
CACTGGGGGCATTGGGGTATCTGGGGAGGTTCTGTGGGGGTGAGAAG  
CAATGGGGGGGGGAGTGGGGGAGGCTGGAAGATTTAGGGGAGGTTAATG  
GGAAGGTCTTGTGGGGCAATTGGGGTAATTCTGGGAAGTGCAGGGGGATC  
CCAGTGTCTCTGTGAGATTCACATACCCCTATACTATCCATGGGGATCA  
CAGTAACCCCTCTGGAACATAAATGGGGGAGAACCCAGGGAGCAATGGGG  
GGCTGTGGTGGATCTGGAGGGGCAATAGGGTGGCCCTGGGGGGCAATATG  
AGGGTCTTAGGGTGCAATGTTGGGGGTCTAGGGGGAAGTAATGGGGGGTC  
TGGGGGCAGTGGTGGGGTCTAGAGGGG

FIGURE 10

SUIITE 20

58/110

Conti224.txt

GGAGGGAGCACTCACCCAGGTCTGAAGCTAGTTTATCTGCAATGAAACAA  
ATAAGAAATGCATGATGAGAAGGGTCAGAATATCATCCCATGGCTGATCC  
CATGGGAAGACCCCGAATCTCTTTGGTTTGCGGAGGAGGACTCACCCAAC  
TGTGCATTCTTCTCTCTGCAAAGGGAAAGCAGAAACAGTGTGTGGTGAG  
AGGAGCAGCTCATCCACACATCGCACAGGAAAACCCCTTTTTTATTTA  
ATTTGGAGGGAGGACTCACCCAGTTCTGAAGCTAGTTTCTTTGCTAAAGA  
AACAGATAAGAAATGCATGATGAGAAGGATCAAATTATCATCCCATAGGA  
ATACCCAGATCTCTTTGGTTAGCGGAGGAAGACTCACCGAATCTGTGT  
TTCTTCTCTCTACAAAAGAAAGGCAGAAACAATGCATGAAGACAGGAGCA  
TCTCGTCCCACAGCTCCCAAAGGAAAACCCCTTTTTTGTTTAATTTAAA  
GGCAGCACTCACCCAGATTTTCAACTAGTGTCTCTGCAAAAAGAAATCAAAT  
AAGAAATGCGTGATGAGAAGGGTCAGAATATCATCCCATGGCTGATCCCA  
TGGGAAGACCTTGAATCTCTTTGGTTTGCGGAGGAGTACCCCAACTTTC  
ATCCCTTCTCTCTGCAAAGGAAAAGCAGAAGCAGTGCGTGATGAACTGAA  
CAGCTCATCCACAGCTCACACAGGCATCCCTCATTTTGTATTTTGTGTTG  
GGAGGGAGGACTTACCCAGTTCTGCAGCTAGTGTCCCTGATAAAGAATCA  
AATAAGAAACGCATGACGAGAAGGCTCAGGTTATCATCCCATGGCTGATC  
CCATGGGAAGTCCCCAAATCTCTTTGGTTTGAGGAGGGGAGACTCACCCAA  
CTTTGCATCCATTCCCTCTGCAAAGGAAAAGCAGAAACAATGCATTATGA  
GATGAATGACTAATTGCACAGCTCCCAAACATTAAAAAATAAATAATAG  
TGGGAAGGGAAACTCATCCACTATCGCAGGTAGTTCTGCTGGAAAAGAAA  
GAGCAGAGCAGTGATGGTCAGAGAGGACAGCTGCTCATCCACAGCTGA  
TGCCATGGGGAGACCCTGAATTCCTCACTTTGGGGAAGGAGACTTACCC  
AACTCTGCATCTTTTCCCTCTGCAAATAGAAGCAAAGGAAATGCATGGT  
CAGAGGGAACACCTTCTCATCCCATGGTTGCTCCCATGCCAATACCCCA  
AATCTTTGTTCTGGTAAG

FIGURE 10  
SUITE 21

59/110  
Conti508.txt

CAGTGACAGTGCAGGTGGAGGGACACGGCGAAGGGACGCTGACGGTGGGT  
GGCTGCATGGACATTGGTGT CATCTCCAAGACCGATGTCCCCTCACAACC  
TCCCCTCATGGTGTCCCCTCATGCTGCCACGGTGTCCCCTGCTGTCCCAT  
CATGGTGT CACGCTGTCCCCAGGTGCTCCGCCAGTTCGCGCTGCTGT CAC  
CTCCGAACGCCACGTGCCAGGCGCTGCACCTGGAGGTGGCCATCACCGGC  
CCCATCCTGTACCATGGT GAGGCCCCACCCAAAGGCCCGCCCCCTTTTC  
CTCGCGGGGGCGGTGCCCTCAACCCCTGTTTTCATATCCCAACCCACAGC  
AGATGAGGACTACGAGGACTACGAGGACTACGAGGAGGCGGAGCCTAAGG  
AGGGGGAGGAGCCTACGGAAGGGGACAGTGCCCCGTGGAAGGGGCGGGGCCA  
GCAGATGACCCCGCCCCCTCAGCCCCGTGTCCTTATGGGATGCCCGTAA  
GCGGCAACGCCGCAGCACACATAACCCCTGCCACGAGGTGGCCTTCCTGG  
TCTGCTTCCGGTGAGGGGCGGAACCTTCTGTCCCTGGGGGCGGGTCTTCC  
TGCTGATGGGCGTGGCCTGTTGTAGGCGGAGCCAGGGGTGGCACTGACT  
GGGATGGCGGTGGTGGAGATCACTCTGCTCAGTGGCTTCTACCCCATAG  
AGCTGACCTGGACAAGGTAGGGGGCCAGGGGGACTTGTGGGACATGTTGG  
GGGGTTGAGGGGAGTTATGGGGTGTGGGGTTTGGGGGTGTTGGAGTTGTT  
GAGGTGGCAGAATGTTTGGGTGGAGTCATGGGATATGGGG

FIGURE 10

SUITE 22



CCACTCTTGGGTGAGCTGACAGCGTCCCACGTCAGCCCCGACTCCGTCCA  
GCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCACGGTGCAGT  
ACAAGGATGCACAAGGCCAGCCACAGGTGGTGCCCGTGGACGGTGGGTG  
CGCACAGTGACCGTGCCCGGGCTGTCGCCGTCCCGCCGCTACAAGTTCAA  
CCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTCCACTGATG  
CTGTACAGGTGAGCATGCTGTGTTCTGCCTCCATGTTCTTTGCTTTCA  
GTGTAGTTGTCTGTGGCAGGAACCTTTCAGGGCCACTTTTGGTTAATGT  
TGCCTTAATAGTCAAGGAAACAATTTGTTCTTGTGAGTGGGAATGCCTA  
ACGGGATGGGAGTTTGGATGATGAGAGGACAAATCTTATAAGGGATGATT  
GATAATTATTGCGGAACGGATGGAAGGAAGGTTGGATGGATGGAATGGTG  
TTTGGATAAATTTGTGCTCAGAGCACAGCTGGAGTGTGGATGAATGTTG  
CTTTGCTTGTGTAATGAGATGGATGTTTGGTTGTGTGGTTGCTTCCACTGA  
GAATTCCTCCCTCTGTGCTGCAGCAGCAGCTCCAGCACAAAGAGGAGCCAC  
CTTCCCCACCACGTCTGGGTGAGCTGACAGCGTCCCATGTGGGCCCCGAC  
TCCGTCCAGCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCAC  
GGTGAGTACAAGGATGCACAAGGCCAGCCACAGGTGGTGCCCGTGGACG  
GTGGGTTGCGCACAGTGACCGTGCCCGGGCTGTCGCCGTCCCGCCGCTAC  
AAGTTCAACCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTC  
CACTGATGCTGTCACAGGTGAGGGCAGGAATTGGCACCTGGTGGGCTCTG  
GGTTTGCAGCAGGTAGAAATGTAAACGTGGCCTGCGCTGGGGATCTTGTT  
TTCCCTGGCAATGGGAACAGCTGTTGGGTGCCTTTTTTGGGAAGGATCC  
CTTAATCGCAGCATGAAGTATGAATGGACCAATTGGGTGTGGGTGGAGTG  
ATGGCTGTTGAGATGAGTTGGTGGCTGCTTGAGTAATTGTCTGTTGGAAT  
GGATGGACAGATATGTGAAGGAGTGAAAGGATGGATAAAGTAATTTAGGA  
ATCGGTGGATGAAGAATGGGTAGGTAGACCCTTGGTGAAGTGGTAGAATG  
GAAGGATTTATGAACAGATATGAGTTAATTCTTGCAATCGAAGTAGGTGTA  
AGTGTCTATTAGCCTGTTGCACTGAACATGCAGTTGCATAGACAAATGAG  
TGGGGAGAAGTACGGAGTAAATCCCTGCATGAATGGTAGGACAGAAACCT  
GAATGCCCTGGATGCTGGCAGTGTGAAGAATGGCACTTGGGATAGATGGTT  
CGAGTATGGGGTAGATTAAAAGATGGATGGAAAAGAGGAACAGAGAGAGG  
GTGATTGGATGAATGGATGGATGGTTGGATGTGACTGATTGACAGGTACC  
AAGCTTTTTTCCTGCACTGTGCCTTCTGTGCTGCAGCTGCAGAAGAGACG  
GAGGAGGAACCACCGTCCAGCCACGCCCTAGGAGAGCTGACGGCATCCCA  
TGTCAGCCCCAACTCCGTCCAGCTGGAATGGAGCATCCCTGAGGGCTCCT  
TTGACTCCTTCACGGTGCAGTACATAGACGTGCAAGGCCAGCCGCAGGAG  
CTGCACTTGATAGTGGGTGCGGCACAGTGACCGTGTCTGGTTTGCTGCC  
ATCC

FIGURE 10

SUITE 23

Conti534.txt<sup>61/110</sup>

GCACAGAAGGAACCGCCATCCCAACCACGCCTGGGTGAGCTGACGGCCTC  
CCACGTCAGCCCCGACTCCGTCCAGCTGGAATGGAGCGTCCCCGAGGGCT  
CCTTTGACTCCTTCACGGTGCAGTACAAGGATGCACAAGGCCAGCCACAG  
GTGGTGCCCGTGGACGGTGGGTGCGCACAGTGACCGTGCCCGGGCTGTC  
GCCGTCCCGCGCTACAAGTTCAACCTGTATGGGGTGTGGGGGCGGAAGC  
GTCTGGGCCCCATGTCCACTGATGCTGTACAGGTGAGCATGCTGTGTTT  
TGCCCTCCATGTTCTTTTGCTTTTCAGTGTAGTTGTCATGTGGCAGGAACCT  
TTCAGGGCCACTTTTGGTTAATGTTGCCTTAATAGTCAAGGAAACAATTT  
GTTCTTGTTGAGTGGGAATGCCTAACGGGATGGGAGTTTGGATGATGAGA  
GGACAAATCTTATAAGGGATGATTGATAATTATTGCGGAACGGATGGAAG  
GAAGGTTGGATGGATGGAATGGTGTGTTGGATAAATTTGTGCTCAGAGCAC  
AGCTGGAGTGTTGGATGAATGTTGCTTTGCTTGTTGAATAGATGGATGTT  
TGGTTGTATGGTTGCTTCCACTGAGAATTCCTCCCTCTGTGCTGCAGCAG  
CAGCTCCAGCACAAGAGGAGCCACCTTCCCCACCACGTCTGGGTGAGCTG  
ACAGCGTCCCATGTGGCCCCGACTCCGTCCAGCTGGAATGGAGCGTCCC  
CGAGGGCTCCTTTGACTCCTTCACGGTGCAGTACAAGGATGCACAAGGCC  
AGCCACAGGTGGTGCCCGTGGACGGTGGGTGCGCACAGTGACCGTGCCC  
GGGCTGTGCGCGTCCCGCGCTACAAGTTCAACCTGTATGGGGTGTGGGG  
GCGGAAGCGTCTGGGCCCCATGTCCACTGATGCTGTACAGGTGAGGGCA  
GGAATTGGCACCTGTTGGGCTCTGGGTTTGCAGCAGGTAGAAATGTAAAC  
GTGGCCTGCGTGGGGATCTTGTTTTCCCCTGGCAATGGGAACAGCTGTT  
GGGTGCCTTTTTTGGGAAGGATCCCTTAATCGCAGCATGAAGTATGAATG  
GACCAATTGGGTGTGGGTGGAGTGATGGCTGTTGAGATGAGTTGGT

FIGURE 10

SUIITE 24

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Conti547.txt

CTGTGTCCCCAACCTGCTTGGTGTTCCTGCGCAGGACACGCTGGTGGCCCTG  
GAGGCGCTGGCCAGATGTGGCTGCACTGGGGCCGTGGGAACACAATGGG  
GCTGAACCTGGGGCTCTCCTGGCCGGGGGGTGGCCGGGGGAGGGCTGGTG  
GCACTCAGGTTATGCTGAAGCCGGGGCTGGAGCCGCTGGAGCAGGAGCTG  
CAGGTGGGGACATGGCGGGATGTGGGGACACGAGGGATGTGAGGACACTG  
GGGACATGTCTGGACTTGGTAGGATGTAACATGAAGACACTGGGGACATG  
GTAGGACATGGGGGACATGAGAACACGGGATGTGGGGGACATGGTAGGAC  
ATGATGGACACAGGGCTTTGGGGTCTTGGGTCTCGCTCTGTCCCCATG  
TCCCCAGGTGCCTCTGGGCAGCCAGTGACAGTGACAGTGAGGTGGAGGGACACG  
GCGAAGGGACGCTGACGGTGGGTGGCTGCATGGACATTGGTGTCTCTCC  
AAGACCGATGTCCCCCTCACAACCTCCCCCTCATGGTGTCCCCCTCATGCTGC  
CACGGTGTCCCCCTGCTGTCCCATCATGGTGTACGCTGTCCCCAGGTGCT  
CCGCCAGTTCGCGCTGCTGTACCTCCGAACGCCACGTGCCAGGCGCTGC  
ACCTGGAGGTGGCCATCACCAGCCCCATCCTGTACCATGGTGAGGCCCCG  
CCCCCTTTTCTCGCGGGGGGGCGTGGCCCTCAACCCTGTTTTGCATATCCC  
AACCCCCAGCAGATGAGGACTACGAGGACTACGAGGACTACGAGGAGGCG  
GAGCCTAAGGAGGGGGAGGAGCCTACGGAAGGGGCAGTGCCCGTGGAAGG  
GGCGGGGGCCAGCAGATGACCCCGCCCCCTCAGCCCCGTGTCTTATGGG  
ATGCCCCGTAAGCGGCAACGCCGAGCACACATAACCCTGCCACGAGGTG  
GCTTCTGCTGCTTCCGGTGAGGGGCGGAACTTCTGTCCCTGGGGG  
CGGTCTTCTGCTGATGGGCGTGGCTTATTGCTGAGGGGCG

FIGURE 10

SUITE 25

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Conti548.txt

CCTCTGCTGCTTCCAGAGCAAAGGAAAAGGGAGAGGGGGGCTCCCACCAC  
CCTATCCCAGAGCATCAGATGGGCAATGGATGCAGCAGCTCCGTGGGTGCG  
TGGAGGTGGCACGTGGCAGGAGCGAGGACGGCTCGGAGATACCGAGGTCA  
TCAGCCACCGAAACCATCTCAGGAAAGGGAATTTCCACACAAAACCTCCAT  
TTGGAGCACCTGGCAGAGAAGCTGAAGCTTTTGGAGCTGGATGGAGACAG  
AGGGGAGAAGGAGAAACTCTGCTCGTGGCGCAAGAGGACATTCCCCTCCA  
ATGGACCACGGGATGATGGAGGTCCCAGTGGAGCCCCCATAAAGGAGTCA  
GTGCAGGAGGATGTGGTCAGCCCTGTGTTATTCCCTAAAGCCCTGTTTAA  
TCCTTCATGTCCATGCTGAAAACCTTCTTCTCTGCGAAGTCCAACACATTG  
CATCTCTTCCCTTCTTTCTCCCATCACAATATCCTCCCCAAACCCCTTTT  
TCTTCCTCCAGGAGCAGATTACAGCGATCTGGAGAACCTCAAGAAACAA  
AAGGAGGAGCTCTTAGAACTCAAAGGAGTGGGGAGAGGCGATGCCAAGA  
CCTTCTGGTAAGAAGCTGTTGCCTTCAAGCTGGAAAAACAGAGGTCTTTT  
TGGGGTCCACGTTGTTGATTTTCCACAACCTACAGACACGGACGGAGGCT  
GAGAGGCAGAAAATTGTGTCAGAATTCCGTCAGCTCCGCCGTTTTCTGAA  
GGAGAAGGAGATGGTGCTCGTGGCACGGCTGGGGGAGCTGGACAGGGCTG  
TGCTGAGGAGGCAGGAGGAGGAGGAG

FIGURE 10

SUIITE 26

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Contig51.txt

AGCCCAGCACTCTGCAGTCTTCTATCAGTTCCAATAGAGGAATTTTGGTG  
GTAGAAGGGGCTGGAAGGACTCACTCTGCTTTGTGGTCTCAGCTGCTGGA  
AAACAAAGCAGAGAAATAGCTGGTCAGCAGGGCAGCTTGGTTTCTGGGGA  
CGTCTCCAGAGGGTCTGGACCTTTCCACCTGCCCCACGGTCCACCCACAT  
TCCTATCTTTCCGCCCCACACCCCTTTTCCCTTTCCTTCATTCCCAATCA  
AACGGCAAATGTTATTTAATGACCACTGTCAATCCCCAGAAAAATCTCCC  
TTTCTCCTGCATACCTCCACGGACCTGAGCTCAGCACCACCCGACCATC  
CCTATCCCTGCTCAACACCTCCCTGTGATCCATCCCCTCCATGCTCAACT  
CACCTTTTCTTCTATAGAGAAAAACAGTGATGACAAATGACCCAACCAGA  
ATTGTGACGATCACAGCCAGAGCCACCTTCAGGGATGGGTGATCTGGGA  
AAAGGGGTCTGGAAAAACATCAGGACAAGGGTTCCTTTTCCATTCCCAT  
AAGTGGAAAAGCAAGACTCAGCCTTGGGACATCACAGAACCCAAAGGGGC  
AGCAACCAGGGAGCAGTGATGCACAATGACGGCATCCCCATATTGGCACA  
GGTGGAGGAGCTGCTCAGCATCGTGTGCCACTGCCACTGAGCCATGGAG  
AAACCCATCCCAGAAATCCAACCCAACCACCTCATCCATGCAGACTTATC  
CACAAATTGCACTGTGCACCTGCTCCAACACCAGCATCTCATGGAACAAT  
TTAGCTCCGACCTCTTCCAAAGGCTGCTGTCTTCAGCTTTCATCCATG  
GATGTGAGGATGAGGATGGACAGAGGTCGGGGTGGGACACACAAACCCAG  
CAACACCTGGAGGCGTCACCCAGCCACTGACCTGACACCTCCAGGTCCA  
CCACAGCGTCTGCA

FIGURE 10

SUITE 27

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Contig99.txt

CCCAGCAAGGCCAAGCGCCGCCATAACGTCAGTGCCGGTGAGACTGTCTG  
ATGCGGTTGCGCGAGGAGAGTCACTGAACATCGGTGATTTAGGCGCAAAG  
TATTTAGCGATTGATTGAGGTTCAATTATGCGGCTTCCTTCTGTGGCTGG  
TGGGTTTTGGTCTGGCTGTGCTTTACTATTGGCGGCATGCTGGCGCGCTT  
AACGCTTTTCGGCCTGGTATCGGGTTATCTCGTCTCTGGTCATGATGGCT  
CCGATTCCAGGCGCGAATTGCATCGCGCTTTGTTGGATAGGTGTCAAGTTA  
TCGGCTTAATCAAGCATTGCTTTGTTGAACAACCGGCGTAGACACCATCA  
CCATCAGAAAAAAGTTCTGCGCCGCCGCCACAGAACGGACACTCAAGCAG  
AAAAGCCCAATGAGGTAGCTTGAGATCGAATATCATTGGTTTCATGCTGC  
CTCCCGCTGTTTCAGTGCTTTGAGCTTGTCGCGGTACTCATCCCGGATCC  
GGATGAAGTCTTCACGGCGGTAGTTGGTCATTTTCGTGGGGACCATTGAGC  
CAGTTGACGTATCCCTGACCGTAACGAGCGACCAACCCAGCTTCGTATTG  
CTGCGCCACGGTCGCTCTTTGGCGGTGTAAGTGGCAGCTCCGGCATTAC  
AGGATTTGCACTGCTTATGGGCGTTGCGTTCTTCAAAGCGCAGTTCAGGG  
TAAGCACCTACTGTCTTGAAATGGCCGCAATCCCACTGGCCACCATGCAG  
ATCAGGCGGATTGGTCTCGCCGCAGCTGATGCATGGCAAATCGGCGTCGC  
GCGCACGGATAAAGGCGTTGAAAGCTTTCTGAGCCTGAGCCTTGTAGTAT  
CCGTCTGGCCTGAGCTCTGCCAGCCGCTCCTTGCGGCGTTTGCGCCCGTC  
CTTTTCAGCCTCTTTTGTCTCTTGATGCGCTTAGCCGCGGCTTTCACCT  
TCTCCTTCTGCGTTCTTCCATTGCGAGGATTGCGCCATGCTCCGGGG

FIGURE 10

SUITE 28

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ContigB5.txt

CCCTATGGGGCCAACCCCGTGGAACCACGCAGGGTTGGGGTTGGATCCT  
CGAGCTCTTTTGCAAAGCCTTTCTGGCTATGGTTGCACTCAGTTAATTAA  
ACTGTCTAAAACCATATTTGTATATAATTAGACATGATGTTTACTGCTT  
CTGTCCCCCCTTGGTTTAAGAGCAGAGAGGCTCTTGCAAGAGGAATTC  
CTCTCACTGAGTGCCACTTTGGAATTGTTGTGTGATCACCCAACTCCAG  
TGCAAAGCCCCAGCCCCACTTTGGGCAGAAATGAATGTGTTTTCTGCTCAG  
AAGAGCTTCGATTTCTGTGCAGCAATGTGGTTGGGATCTGATCACTCAC  
CGCACACGCTGAGCCCTGTCAACAGCAGCAGCAGCAGCAGCAGCAGCACC  
CCCAGCATGCAGGCTTTCTGGAAGTCCCACGGAAGTGAAGAGCCCACAC  
TTATATAAAACAGACATTTTGAAGAACTTTTCTTTTACAGAAATGATC  
TCCCTGTGAAAGAGCCCCCTCCACCAACCTGCTACGTTAGAGCAGAAGTTG  
ATGGCTGCTTTGGTTTCTTGAGAATTTGGGGTCCCCGACCCCTTCCCATT  
GGTTCCCATGCTGTGTATGAGCAGAAGTTGATGCCTGTTTGTCTTCTCC  
AGTTCCGGGGTCCCCCTGGACCCCTTCCAGTGGCTCCCAGTGGTTCCCAGC  
TGGGAAGGAGGTGGCACAGAGGGGTGACAGCAGCAGGAGCATGGGATGG  
GCTCCCGCTGGAGGTCAGATGGACACAGGGACATCACCTCCACGCGTGGT  
TCTGGAGGTGGTGGAGGCCCTGCAGGCTCCATAGAGCATGGGGTGGAAGC  
TGAGCAGCCCCCAGGCTTTGTGAGCCGAGCCCAGTGTGGGGCAGCCGGTG  
GCTGGGAGGGCGGGGATGTCTGCAGCCCTCATGCCACGTGGATGCAGGGT  
GCGTTTGCCACCATTTTATTCCATTCTCTCACATTGGGCTTCCCGATCTG  
GGCTGATTTTGTCTCAAACACACACCTCTGGCCATTCCCAGGCTTCC  
TTCTCCCCCAGCCCTTCTTTACTCCCCATACAAGCCAGGGTGGACCCA  
GAACCCAACCAGCATTGCTGGTGTCTCTCA

FIGURE 10

SUITE 29

CCGGCATCACCGGCGCCACAGGTGCGGTTGCTGGCGCCTATATCGCCGAC  
ATCACCGATGGGGAAGATCGGGCTCGCCACTTCGGGCTCATGAGCGCTTG  
TTTCGGCGTGGGTATGGTGGCAGGCCCCGTGGCCGGGGGACTGTTGGGCG  
CCATCTCCTTGCGATGCACCATTCTTTGCGGCGGCGGTGCTCAACGGCCTC  
AACCTACTACTGGGCTGCTTCTTAATGCAGGAGTCGCATAAGGGGCATCGG  
TCGACGGGATCACGTTGTGTCCCTGAAGCTCTCCTGTACCCAAACACAAA  
GGTGATGTCCCAGCATCCCTATCCCAGCACTCTGGGGGACTCCTATTGA  
ATTCTCTCTTGGGCTTGCTGCCTTCTCTTCCCGTTCCCAGAGATCCCAA  
AGGTTAAGCACCTTTGGGTGAGTGTTCAGAATTGTCACTGCCAGTTTGG  
GGTATCAGTGGCAAATTGAGACCCCTTTTACCCAATCTTGCACTCTCTGG  
TTCCCCAGTCTTATGGTTTTAGATGGAGTAAAAAGGTTTATATGTCATAA  
AGTTCTTCTGTGTCTGTTATTCTGCTGCTTCTGGATGCCAGGATCATGGG  
GATAAGGGGAAAAACAATGGGTTCTCTTATGCGTAGAGATGCAATCAGATG  
GGGAGAAAAAGAAATCTTAATCTTCTGATCCATCTGACAGATATTCAGT  
ACAGCCCTGAGGATGTGGGAAATAAATCTGAAGAGTTTGTGGCAGTTCC  
AAGGATTTGGAATGACTAAATCCCATTCCTGGTGTCTGCACAAAGTTGGC  
TGTGTTGGAACCCAGAAAGATCCATGCAAGTGGGTGATCCCTGAAAGCAT  
TGTGTTCTGCTGTCTGCTAGCGGAGAGAAAGACACAGAGGGGAAAAATTAA  
GTGTTTTATTGTTAATTATTGTACACTCTGAGGTTTCAAATACCAAATCT  
TTAACGAGAGCGGACCACTTGATTTGAGGGTGACCATCTCAGATGGGGAC  
AACTGTACCTGATCAGGCAAACCTGGGGGAAATTTGCCTTTCTGCCACTC  
TTTGGGTGGGATTTTCCCTTTTGACCACCATTTTCTACATTCTAATCAC  
CCATTCAGCACTTCTCCCCCTTTTTTTTGCCCCATTTTTCTCCTGCTCA  
GCACTTCTTAACAATATAATATAAATCAATATCATATCAATATGATTCTA  
TGCCAATAGATTAATGGGGATGAAAGACACATAAAAACCCAAGTCCTCAT  
TTCATCTGCTTCCCATGGGATGGGTGGGAGGTGGCTGTCCCCTGAGGCT  
GTAGGATGTGGGGTCACCCCTTGTCTGTGTCTCAGGGACACAGCCTCAGCT  
TGGACCTGACCCCTACCACCCACAGCCACGGACGGACCCCTCTCCCCAGAG  
AAGGATGCATGGGAAAAAACAAGATGAGCCCCCTTCATCAGCATCAAA  
AAATGCCACCGTCCCTCCAGCGTAGTCCAAGTGGACGCTGACCTCCTGG  
GCACCCAGCGCAGAGCTAACAGGGTCACTTGTGGGTGGTGAAGTCCCGG  
ACCTGTCCCCCCTTTCTCCACCCCCCAAATCCCCCTTTGGGACAGAG  
GCTGAGTTGACCTTCCGAGGGATGGATTCTCGGGCCACACCGATGGCCC  
AGTCCCCCTTCATCCCCCACTTCCACCTCCAGCAGTGCCGCGCGGCAGAG  
AAGCTTTGGTGGCCCAAAACAAGGGCCAGTAGGCGAATCTTTCGGGTT  
ATCAGGAAGGTCTGTGTCTTCCCCACGTTTCACTCTTTCGGTCTT  
CGGAGAGGATGAGGTCAGGGTGAGCGGTGTGGGGTCCAGGGTGATGCTG  
GCTGTGGGGTGGAGAGGATGAGGAGTGTAAAGTTTGGGTCTCGGTGCTG  
AGGCCATGAGGATGCGGAGAGCTTGGATCTCCAGCACTAAAGGAGTTGGA  
TGTGCTCTAGATGGCCCCACCTGAGTAGGGTTGTAGGGTGGGACCGTCCC  
TTCCAACCTCAGCCATTCTGTGGGGCCATGGGTTGGCATCGGAAGGGTAA  
AAAGTACCAAAGAAGAAAGTAAAAAGGTGAGAGGTGGAACCCCTCTCAT  
GTGCCCGTGCTATATGACAATAAAAGTGTTTTGGAGCCCCAGAATGCCCA  
GAAATAAAGGCGTTTCTGCAGACCTTCTGTTCCATTGGTCAAAGAAATG  
GTGAGGGGAATAAAAATGGAAGGAAGGAGATCTATGGGATATTACCTGCA  
AAGTCTGCAGTGCTTCATCTCCTAGACCAACCCGGACAGTTTCAGCCAAC  
CCCATGGTTTAAAAAACAGAGCTGAAATCTGAAGGCAGGGATAATGAATG  
AGTTCAACCCGCTCACCATATTTGTTTATGGGAAATGGATATTTATCAAG  
GCGAGGGATCTGCCCTGGGGCCATCATCCCAATTACAGCCAGACTCGGC  
CTGCAGGGTGAAGAAAACCTGTTTGGCTGCCCTGATTTTTGTGTATTCTC  
CCCTCGGCATCTATTTTTGTCCATTTGGGTACAGCCTATGGGTCCAGGCG  
CGCCTCCATCTAACAGGTAATGCGGCTTTAGGTTCTCATGCTCAGCAAAA  
GGCACTTTTAGGAAAGGTGAAGCTGGAGGGGTGCAGAGCCGGAGAGCAGC  
CCGTCTTACCCCTGAGCACTTCTCAGGAATTACAGCAAAACGTGTAAT  
TAAGAGTGGCAAACGGGGTATCGAGTCCTTCGGGTCTCAATTATTTTCT

FIGURE 10

SUITE 30



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COSMIDE.txt

GAGTGGGAATAACCCGTTGCTCTTCCATCTCTCTGCATTATTCTGCTGCA  
GAACGAGTGATGGGCTGCTGGTTTTTACC AAAATACCACCATTTCACCACC  
CGAAACCCCTTCTGAGTACCTTGAAGCCTCTTCAGGGTTTTCTTCAGAGCA  
CCGTTCTCCATGAGGAATGGCACAGCCTCTCCTCCGGCCCTGGAGAAGC  
GCCCCGCTGGCAGCTGGAAGGTCACTTTTCCACACCTGGAGGGGAAATAAA  
TGCATTTTCAGGTGGTTGTATCACAGAGCATGCCATCACTTCAGGACAGC  
AGAGGCCAGCACACGGCGGCCATCCCCAAAATACCCTTCAGGGCTCGCAG  
TTCCCCTGGAGCAGAAGAGCATTATTGATGAGCTTTCTCCTCCATGGTC  
ACTGCTGATGCAAGCTCACAGAACAGCTTTTCAGAGAGGCCACATACC  
TGGTGATGGGGCTTTTACATCCTGGGGACAGAAGAGAGAGGGGGAGAG  
GAAACTCAGGTGAGTGCATGACCCATTTTGTCTTTAAAGTATGGAATAAT  
GAGCTGTTTGAAGTGGGGGTGGACCTCTTGGGTCTTCCAACATGTGCCAA  
TTTTGACTTTAAGTCATAGAAAAGTGAATTGTTTGAAGTGGGGATGGATC  
TGTTGGGTCTTTCAACACATGGTCCATTTTGTCTTTAAATCATAGAAATA  
AAGAATTGTTTGACCAGAGATGGACCTCTGGGGTCTTCTCCACGAGGAA  
GGTGAACCAACTGAGGAGCATCCATGCACGGCAATGAATCCTGCAGATCC  
ACCCCACTGCTGCTCTCCCAACCCAGCCGTGGATTTCCTCTTTAAACA  
GACCCCATGAGGACCTTCTGCAGTAAGGTGAAAATACTGGGAATACTGAG  
ATGAGGATAAAACGGTGGGGGGAAAGAGGAGGCTGCAACCTCCATCTCC  
TCATTGTGGTGGGGGTTTTAGGCTGATGGAACGGCATAAAATGGGAGGAA  
AACACCCAATTAAGGCACCATGCAATTGGTCCGGGTGGGGAGGACATCCC  
TAAAGGACTTTTCCCCTTGAAAAGCTTCCCTGGAGGAATCACTCACCG  
ACTGCTGGCTCTTCTCTCCTGTGCTTTTCTATCCAGCGGGGAAATCTCC  
TCCGAGTGCTTGGCGGTGCTTTTCTGCTCTTCTCAATCTCATTCTTTCAG  
GTCTTCCAGCTGCCAGAGCAAGAAGGGCTCTGTGTTTTCTGCTGGAAT  
CTGAGCCCTCCCTACTGGGGCTCAGCTTTCTTCTGATGCAGAAAGTGGAA  
AAATAAAGAGCAGTGGGACTGGAAATACCAGGGGGGACTCATGAGTGGCA  
TCCCCCACTGGAGGAGCTCAATGGTGAGCTGGAATCCTTGTAAGTTTA  
TCCAATGTGGGGGACAGGAGGAAGAAATCAAACCAAAAAGTCATGAACA  
GGTGGCTGTGAATTCGGGGCAGAAAGCTGAGGGCCCTAAAAGCACAGGAG  
GCAAAAAGGATGGAGAGAAACGACCCCTACTGATGACACATCGCTGCCAG  
CAGCTGACACCTACCAGATCCTCCAGGTTTGGGCACTCCAGGGCGCTCTT  
CTTCTCGGAGACTTTCTCTCTCCTCCTTTGGAAACCCCTGATATCCCTC  
TGAGTTTCTTCCCCAGTGAACCCACAGAACCTGTTGTTTTAGCCCTTG  
ATGGGGTTGGGGTTTTCCCTTCTGTTCTTCCAGTCTGGGGTAGAGCT  
ATGGGATGGCTGCGTTGAGCCTGCAGGTCTGCTCCTGGTGGCACCCCTTG  
CAGGGCGTGCTGGGAGCTCTGGGTTTGTCTTTGTCTTTCTCCAGTTCC  
TTGTTCCCGGGGAGATGCTGAACAATGTCACTTTGCAGATTTTGTGAGCTT  
CCTTTTAGGATCGAGCCATCGGGAGTGGGGTTAGGGGGTGTATATGGGGA  
AACCATAAGGAAATAGGGAAGGAGATGCACAGCCGGATCCTTGTTGGGGAT  
GTGGAGGAGCACAAAGTGAAGATCTTGGGATTTGAGTGCTCTCTCAGCCC  
AGCACTAACACAGAGCACTCACAGCCCTGGCTCTGAGCTCTCGAGGAAAC  
ATTTCCAACCATTTCTGCCCCACTGTCCTTGTGTTGAGCCCCATGGCCAA  
ATACACATGCCTAGAAAATAAAGCCATGCATTACATATGTATTTAATTTT  
TGCGTGGCAACCACTGAGACCAACTGGAGGAGATAACTGCCATTCACTT  
GGGCAGGTTTTGCAGGGGTGAACCTGCACTTCCAGCAAAACCTCCCTGTTGG  
GAAGAGCCACAGGGATGGATGGCACTCTGGGAGCTGAAGAAGTGAAGCA  
AACTCCCTGCAACCGCTCCCCTGGGGCACAGAGCCTTTTCATCCAAAATA  
AGCGTCCATCATTGAGCAAATGAGTCAACCGTTGGGCAAACGACTTGC  
ATTGCATCCCGAAAAGCATTAAATGCAGAGCCTGGAAAAGTAGCTGGGCT  
GGAAACATCTGCATTGCAGATCTATGGAGCAGAATAGACCCTGAACAGAT  
CCTTCACCCAAATTCAGCAGGTGGGACCAATGGCAGCGATGCGTGG  
GGCTGAGGAAAGATACCAACACATCAAAGAGCAATATTGAAATTCAGCT  
GTAGGTTTGAACCTTTGGAGGTGGTGAGGTGGGGCTTTGTATGGGATACC  
CACTCATATCG

FEUILLE DE REMPLACEMENT (REGLE 28) CCTCCC

FIGURE 10

SUITE 31

69/110

COSMIDE.txt

ACCCTCTTTTGTAGTTCCTCTTCTGGTTCTACAATCACCAACCTGTGTGTA  
TTTTGGTGCTGCCTGTTCTTCTTTGGGCTTTCTCAGAAGAAAATGGGTT  
TTTGAGGGAATCCATTAGGTGAGTCCTCACCCCAAGCAGCTCTTCTTCA  
CTTTGTTGGCCCAAAGCTGACCCAGAGCCATACCCCAAAGCAAACCCAG  
AGCCGTACACCCATAATGAGGCAGGAAGTGGAGTGTGCAGAGCACATCTT  
TTAATTAAATTAATATCAGAAACGTAGGCAGAGACCAGCTCCCCACAC  
CAGGCGTTGCTATTTGCAGTGAAAGGCCGCATACCTTTGCAGGACACCCC  
AGATCTGCCCCACGATTGATGTCAAATAGATGCATAAATTCCTTCCAAG  
TCTTCAGTGCTCTCTGGTGGTTTCCCCACCCTGCAGAGGGACCGCCCCGG  
GGCTCCCAATGGGGACAGACACAGGGCAGAGCAGCGGGTCCCCTTGGCAC  
ATTGCTCCAAGCAACCACAGCACACATCCCATCAGATGCCCTTTTCATAA  
AGGACATCTCAAGGACAGATCTTTAGGGGAGATCTAAACCCAAACCAATC  
CAAATGGGACATCAGCTGCCACTCGTGGACTGCTCCTCTGAGGGGGGAT  
TTTGGGTGATCTCTTGAAGCGAGCCCCAGCCCTATCTTGAACAAGGGG  
AGGACCTTCTCCCCATTGAACAAAGCCCTGGTGTACACCAAGATGGGGGT  
GTCATCATCCGAGCTGAAGAATGCCACCCGACCCCTTCGTAGTCCAGGG  
AGACCCGAATCCTCCTGGGAAGTGCATTAGACGTAGGTTGGCACGGGGA  
GACGTGAGGGAGTGGTAGGCCTCCAGCGCCAGACACCTCTTTGGGGCT  
GAAGCTCATGGGTCCCTTCTCTTCATCGAAGCCCGGGCCACCCAGGG  
CCCACACCCCCCTGTCCCACCTCCACCTCCAGAAATGCCTCCCCGAG  
GTGAAGCCCTGGCAGCCCAACACGCAGGGCTCGAAGCTGAACCTCTCGGG  
GTTCTCGGGGAGGTCTGTGGCACCAGTTGGCCCCGGGCTTGTTCGGT  
CTTCAGAGAGATGGAGGTGGGGTGAGCGGTGGTGGGGTCCATGGTGACG  
TTGGCTGTGGGACATGAGGGGGAATGGAGGTAGGATTTAGGCTTGGGGGG  
AGCTGGAGAGGTTCTCTCTCTCTGTCTCTTTCTCTGGGTGCTTTTGA  
CATGGGCTGGTGGTGGTGGTGGGTGATGGTGGGCTGGGTGATCTTTGG  
GGTCTTTTCCAACCTTTGTGATTCTATGGGGTGTGTGGGGCTCCACCAGC  
CTCAGTGTCCCCCAGTAGAGATGTAGGAGAATGGGGAGAGGACAAATTTT  
AGGGCAGCATAATGCGGGAGGGACAAAGACATGGGAAGGGGACAGCTTGA  
CATTACGGAGGGGAAGGGGAAGCACAACACTGTTAGGTTTTGCCTTGA  
ATCTGTTACTGGCTTTGTAGGACCACCAGCATCAGGATGCTGTCCCCATT  
CCCTCCCTTCCCTGTGGGACTGCGTTGTTTTTCCCAAGAAACCACTCC  
CCACCCACATCCACCCTGCTGACATACCTGGCTCTTGCAATTGAAACA  
TCAGGCTGTCTGAAAAGGAGAACAAATTCATGCTATTGGGTTTATGCTTC  
AGGAAAAGGGGCTGGGAGATGGGGAAGGGAACCATGGGGGTCTGGGGGC  
TTCGCAGTGCAAAAGCTCTGGGTTTACTGCAAGAGCCCCACGACCTCCC  
AGACCTGGAGGAGACCCGACCCCATTCAGTACCTTGGCACTTCTGCAGC  
GTCAGTCTCACCAGGACGTTCTTCTGAAGGAAGTCCCTCCAACCTTCTTTC  
CAGAGTGGGGGAAATCTCTGCTGGAGGGCTGAACCTCATCATCTCACAGC  
TGCAAAGAGAGGAGAAGGGTGGGGATGGGGGGACTGTTGCGTTGGTTGGT  
TGGCTGTTTATTTTATTCTCAATAGGAGAAGCTATGGGGTGAGGATATTT  
GCACAGGGACGAAATCCCTTTCCCCCTGGGATCCCTCTGCCTTGCAGCC  
CTCCCCCAGGGTGCCATCCAAAATCAGGGTGACAATAGGAAGGAGCCAT  
GTTACCTATTCAAGAGCCTCCTGATGTCTAAAGGTGGGAGGAGAGGGA  
GAGATGGATCAGAAGAGGAGACCAAGGGCTGCCCTTCGTATGGCAATG  
CACGCAAAAGACCACCTGCCCACGGTGTGATCCCCCAGCAGCAACAC  
AGGGAGCTCCCATGGGGTTGAGTTTGGGTTCTCAGGGTTTGCTCTGTCCC  
CCCATTTCCCACCACCCCTTTGGGTTCTCACCAGCAGGAATTTGCTGTCCG  
GGCTGCTGGAATTTGCCCTCCATCTCCAGATCAGGGTGTCAAGGTGGGA  
CATCTCCTCCATCACCTTCGTACCGCATCCTCCTGTACTTTGGTGACGG  
CTCTGTCCAGGTCTGCCAGCTGGACCAGCAGGAAGCGCTCCTTCTCCTTC  
AGAAATCGCTGCAACTGCTCGAATTCACACACTATCCTCTTCCCTTCCCTT  
CTTGGTTTCTCCTGTGGGATGAGGGAGAAAGCCAATGGGGTGGAATAG  
AGGCAGGAAGACCCCCCTGGGGTCTCAGGATGCCGTGTTCTGGGGGATA  
TCCAACCAAAACCAATGGGATCTAACCAATGCCAATGGGAGCACAAAC

FIGURE 10

SUITE 32

FEUILLE DE REMPLACEMENT (REGLE 26)

COSMIDE.txt

70/110

ACTAATGCCAATGGGAATTTATCACCAGTGCCAATGGGAACGTAACAACA  
GCGCCAATGGGAACGTAACACCAGTGCCAGTGGGAATTTATCACCAGTGC  
CAATGGGAACCTTAACATCAAAAAGCCAAAGATCATCTTGCTGGGCATTTG  
GGAGCAGCAGGAATTTTTAGGAGTTTTATCCCAAAGCAAAACCAAAGG  
AGGGGGTAGGAGATGAGCTCTGTATGAGGGATATTTACAGAGTTTAGGAG  
GATCTGCTACGTTATCTCTTTAACACAGGGGTTCCTGCGTAACCCAGCT  
GATAAACACAGCCTTAGCGCTTTCCAGCCCAGCTGCGAGCCAAAATGC  
ATGATCTGCCCCCAAATACACCAAAACAAAACAGGACAGGGCGGAGGGGA  
AGGCAGACACCTCCCCTGCTGCACCCACCAAATACAAGCCCGTCCTTCCA  
CCAGTCTTCTGCTTTCCAGGTACTTTTCCCTCTCCTCCTTGAAGCCTG  
GAGGCGAGCCTGAATTTCTTCTGTGCCAAAAGAAGAAAGGCGGAAAGCC  
TGTTTTCCCACTTAACTGCTTCTGTGATGAGGAGAGGCTTGCTAAAG  
CCTGGAATCCTCTGCAAGGTGCAGAGCTGGGCAGAGGGAAGCTCTGTGAG  
CACGGTGTGCTGCTCTGGAGCTCTGTGCAAGCTGGGAGTATTTGCAGAG  
AGAAAAGAGGGGAGAAAGGGAAGGAAAAACAGAACTTGCTGCAAAACGTAG  
AGAAAAACGCTGCAAAAGAGCAACAAAAAATCAGCACTGACAGCTGCGC  
AAGGAGGTGTGGAAGGGCAAGATAAGCACTTGGTGAGATTTCCCTCATAA  
ACACCCCAAAACGGCGGCCCTGGGGTGTGTTTCTGTATTTAAGAGCCCTC  
AGTGGAATGGTTTTTGCAGGGCTGTGGTGAAGAGCAAAGCATCAAAGGA  
AGGAGAGGGCAGTAATGTTGCAAAGGGCTGACGGCGGTGGTTGCAAAGAG  
GGAGGATGGGGGGGGATGCGCCAAGCAAAGGGTTGCGTGGGTTCAACCGC  
AGGGATGCACTGCGCCCTTGGCTCCGGGTTTTGGGACCGTACCTTGTA  
CCTGGGCGCCTGGTGGGCAGGGAGCACAGCTGGGAGCGGTGCGCCTGG  
GACGCTGCGACTGCGCGCAGATAGGCTCTTGGTCTCTGTGCAAGAGAG  
CTTCAGAGCCTCGCGGTGCTGCTTGACCAACCCGAGGAATGCAAACTCA  
GCTGCCGGGCGATGCTGGCGATATTTGCCAGCTCTCTGCTGGGGCGGAAA  
TTTTTGTGCAACGCCGTTTTCTGCACTGCGGACAGGGGAAATTTCCCTC  
CAGCCCTTCCAGCAGCGGGCGATGCACTCCCGGCAGAAAGTTGTGGCCGC  
AGGGGATGGAGACGGGATCCTGGAAGTAACCCAGGCAGATGGAGCAGGAG  
GCTTCGCTCTGCAGGCTGTCCAAGGGGCTCTGCGTGGCCATGGGCTTCCT  
TCTGGGCTCCGATCCGCAGAGGGAATAGGGGACCTTTCCCTCCTTATCTCC  
TCGCTGATAGGAGAAATCCGGCCCCGGAGGCTGAGCCTGAGCCAAACAGG  
GCTGGGAGAGCTCAGCCCATAGGGGATGCTGGTGGGAATGGGGGAGCTC  
GCGGCTCCCCAGCACGGAGTCACCAAACTGGGGGGATCTGGGGGAAATTC  
GGAGGAAAAGTCAGATTTTGTCTCTCCTCGAGCAGCAAAGAGGGCAGGG  
GAGGCGATTTTTCCCTTCTGTGCGATCACTGTAAGGAATTTCCAAAGAAA  
ACGCATGGAGGTCTGCTTGTGGGATGGAATATAGACGTATATTGGAATA  
AATACAGGAAGACGTTGGAACATGGGAAGGCACTGAGATATAAGCGTGCT  
GTGTTGGATATGACTCTGCTCGACTAAAGTGAAGGTGGTTTTAATAGCAC  
TGCTCAGAGCCAGGCGGGTTTTGGTGTGTTTTGGGGGAATTACGTGGGT  
TTGGAATTGGGAAATATGAGACGGAAAAATAAGAATAATGGAAGCGCCCA  
ACGTGGGGCTCGAACCACGACCCTGAGATTAAGAGTCTCATGCTCTACC  
GACTGAGCTAGCCGGGCTGATGGGCACGCACCCTTCTAAGCAATACTTCA  
TGGTGATCCTGCGGAGGGGTGCTAATAATTCTACCTAATTATTTGTAA  
TTATCCCGGTAATTATGGGTCTTGAGCAATCGCAATCCACGGGGAAAGAG  
CTGTTGGGGAAGAACCTATCCCTACGGGAATAGCCGGGAACTGCCC  
GGCAGTGCTGCAGGGCGGGGAAAGAGGGGAAAGCAGGAAAAAATGGG  
CAAAATGGAACGTTTAAAGTGGAGAAATTAACAGTGAAAAAATGCAGG  
AAGCGTAAAGTAAAGGCTGTGTTTCTGCCCCGTTTTGAACCGGGGACCT  
TTCGCGTGTGAGGCGAACGTGATAACCACTACACTACAGAAACGCGCTGA  
AGGCCGCTTCGCGCACGGAGATGTGAAGGGGCGAATGCCGGGGCTCGGT  
GCGGAGTTTGCAGATAGGGGCGGCTCCGGGCGGCTCCCGCGCGGTTCCG  
GTGAGCACAGAGTGACGCGGGTGACAAAATGAAGGGAATAATGTAAACT  
GATGCTCCCGAATCGAGGCTCGAACCAGCATTTGTCGACTGACAGCCGCG  
CGCTCTACCGAATCGAACCAGCATTTGTCGACTGACAGCCGCG

FIGURE 10

SUITE 33

FEUILLE DE REMPLACEMENT (REGLE 26)

COSMIDE.txt 71/110

CCGTAGAGCGCCACCCCGTTGCCTAGTGACAGGAGCGCCGCTTCCGGTC  
AAGTGATGAGCGGAGGGGGCGTGGCTTGTGTGATAGGACGGAAGTTCC  
GGTCAGGTGGTACTGGAAGGGGGCGTGGCTTGCGGCAAAGGGGACGGAA  
AGCGGAAGTGCTGCCGTTGGTTGGCGGAGTTCCGACCATAGAAGAACGAC  
GGCGGCGGTGGGAGGGCGGGAGGTAGAGCGGTCCCCGGGGAGAGTGCTGA  
GGGGAGCGGCGAGGCCCGAGGAGGGAGCGGAGCTTACGGGGAGTGCGGAG  
CCTCGAGGCGGGTCCCAGCGCTTCGCTGTGGGGCAGGAGAAAGGCTTCGG  
GGCAGGAGGAAGAGGGCCTCGGGGCGCTGAAACCGGTGGAGACGCTGCAGGAGGAG  
ATGGGGCGCTCGTGGGGCGGCTGAAACCGGTGGAGACGCTGCAGGAGGAG  
GCGATCTGCGCCATCTGCCTGGACTACTTCTGAGGAGCGGTGTCGATCGG  
CTGCGGGCACAACTTCTGCCGGGTGTGCATCGCGCAGCTGTGGGGTGGAG  
GAGAGGCTGAGGTGGAGGAGAGCGGCGGGGCCGCGGCTTGGAGGAGGAA  
GAGGAAGAGCTGGAGGAAGAGGAGGAAGATGAGCTGGGGGAGGAAGAGCT  
GGACGTGGAGCAGGAGGAGGAGGAGGAGGATGGAGGCGGGGAGGAGGAGG  
AGGAGGACGACATGTGGAGCGAGGAGGAAGAGGATGGAGAGCTGTGGGAA  
GGTACTGGGGGTGGGTTGGGCCTGCCCTGTTGAGTGTCTTTATGGATGA  
GTGAGGGAATTGGGTGCACCCTCAGTCAGTTTGCAGATGATGCTAAGCTG  
GGGGGGTGTACTGATCTGCCCTGAGGGTAGGACGGCCCTACGGTGGGGTCT  
GGACTGGGCCGATGGGCTGAGGGCAATGGGGTGGAGTTCAGAAGGACCG  
AGTGCCTGGTTCTGCACTGAGGTCAACAACCCCATGCAGCTCTACCTG  
GGGTAGAGCGGCTGAAAGCTGTGTGAGGGAAAAGGATTTGGGGGTGAATA  
TGAGCCAGCAAGAGGCCAAGAAGGCCCATGGCATCTGGCTTGTATCAGA  
AATAGAGCAGCTAGTGGGAGCAGGAAGTGACTGTCACTCTGTACTGGCAC  
ACCTCAATGCTGCACCCAGTTCTGGGTCCCCTCTCACTACAAGAAAGACA  
TTGAGGCCAGTGAGGATGGTGGGGGTTGACTCAATGATCCCTGAGGTT  
TTTTCCAACCTTGATGATTCTGTGATTCTCAGACCCCGTGAAGAGGAGC  
TGTGGGATGGAGTGGTGCAGGGAGAATCTACTTTGGGGACGATGATTAT  
GATGAGGATGTGATGGAGGAGGATGTGGAGGAAGAGGAGGAGGAGGAGGA  
TGAAGCGCAGAGCCCTCCGCCCCCTGTCTGCTGCCCGCCCTCGCCGCC  
TGCAGACCTTCACCTGCCCCCAGTGCCGCAAACCTTTTCCAGAGGAAT  
TTCAGACCCAACCTCCAGTTGGCAAACATGGTGCAGATCATCCGGCAGCT  
CCACCCGCACCCGCAGCGCCTCGCGCCGCCCGCCGGCCCTCAGCCTCAG  
GGGGTCTGGGGGAACCCAGGGATCTGGTGGCAACAGGAGGTGGGGG  
TGTCCGAATCTGTGCGAGAAGCACCAGGAACCCCTGAAGCTGTTCTGTGA  
GGTGGATGAGCAGGCATCTGCGTGGTGTGCAGGGAGTCACGGAGCCACA  
AGCATCACAGTGTGTGCCCTGGAGGAAGTCGTGCAGGATTATAAGGTG  
GAGTTTGGGAAGGGTCACGGTGGGATAGTGGGTGAGGTGGGGTTTGGGG  
AAGGGCTGTGGTGGAGAAGGCGGGGTTGAGGGAAGAGTTATGGGAGAGT  
GGAGGCTTGAAGGGAAAGTGAGGTTGGGATCAAGCTAGGTTTCGTCTTGCT  
GAGCTGGTTGGGTTGGAGGCGTGGGAGGCTGGGAAACCACACACTGCAAT  
GAGGAGGTGGAAGGCTCTGGGTACCCATTTCTGCTTAAAAACACCTTCC  
CAGCACAGTTCCTCAGAGAAAAGCAAAGGGAAGTGGCGTGAAAGTTGGCT  
CTGAGGTTCCGTTTTCAGCTCTGCCACCAAATTAGGGACAAAAGAGGCG  
ATGACAGAGGGGATGCCCCAGGCAGGTTTGTGCTGAGTTGTGTTTCTTTC  
CCTCAGTACAACTCCAGAGCCATTTGGAGCCACTGAAGAAGAAGCTGGA  
CGCGGTGCTGAAGCAGAAGTCGAATGAGCAGGAGAAGATCACAGAGCTGA  
GGGTAAGAGCTGAAGGTTTCTGTGCTTCATAGAATCATACAGGAGAACCA  
TCAGGGTTGGAAGAGACCACAAAGATCATCAGTTCCAACCATCACCGCTG  
CTGGGAGTGTGCCTTGGTGGCTGAGCAAGGAGAGAGAAGCTTGTGCTG  
CTCTGAGCTCTCAGGAGGCATCATATTCCCTTTCCTGCAATTATTGGGC  
TGTGAGGCTTGGAAACGGTTTCCAGTTGAATTAGAGCTTAATGAGAGC  
TTTGTGTGCTCAGTGTTGAGTGGGAATTEGTGGTTTGGGAGCTGGTATT  
CCTCATTGTAGTTGAGGATGCTCTACATCTCTAAACCTGTGCAGACTTTG  
CTCAGTTCTGTCTGTGGTGCATTGAGGAGATGCGTAAGCTTATGGTGTGT  
GGTGAAACTGAGAGAAGCATAGCACAGCAGCCCAAAATGAGCTGATCTC

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

SUITE 34

TCACCTCCCCCTTCTGCAGCAATTCCCCTAATGCTTTTCTCCCTCTGCA  
GGAAAAGATGAAGCTGGAAATCAAGGAATTTGAGTCTGATTTTGAGCTGC  
TCCACCAGTTCTCTATTGGGGAGCACGTGCTGCTGCTGCACCAGCTGGAG  
GAGCGCTACGAGAGCCTGCTGGCCCCGAGAGCAGCAACATCAGCCAGCT  
GGAGGAGCAGAGTGCAGCCCTTAGCCGCTTATCACGGAGGCAGAAGATA  
AGAGCAAGCAGGACGGGCTACAGCTGCTCAAGGTCTTCTTCCATCCCTTT  
CCTTGTCTTTATGGCAAAGCGATAGCACGATGGTGGGAATAATGCTCCAG  
AAAGCTTCTGTGTCATGAGAGAGTGCCTTTAGTTGGTGGGCTGGGTGCTT  
CTCCACCCCTCCTTGTGGTGGTTTTTGAGGGAAAATGCCGGGGGGGGGG  
GGGGGGGGGATATGCCCTGAGAGATTTAGGGTCTGTTTTGGTAAGGAAAG  
CCTCCAGCAATGTGTGGGCTGTGTCTTTGTTCTGTGGGGAAGGGAATC  
ATCCAGGCTCAGTGTGAGTTGTGGCTGATAAGAGGATTTATTGGGAGCA  
ACGGTGGGATTGGTATCAGTCATCCCTAATCCTTTCTTCTTTCCCAC  
CTTGCTGCCTCCTTCCCACAGGACATCAAGGGCACTTTTATCAGGTCACT  
GACTTTGTTTGCATCTTTTCACTTTGAATAACTTTTCTTTTAAATGT  
CAAAAAGCATTGAGCTTTTGTTTAAATCCTGTGTGATGGGTACAGTT  
GGGGCCTGGTAATGCAGGGGAAAGCTGTGTCCTAACTTTTGGGTGATGGA  
AACTTCTGGCTGATGGGGTGCAAATGGGATCTGGGGAACAACCTGGGAAA  
AGACTTGGGAACCTGGGAAACAACCTCTGGGGCCATTGGGAAAGGGGAAG  
GGTGGGGAGGAGATCTCGGCCCTGATTTCTGGAAGCGTGGGTGTGCCCAT  
GCAGACCTCATGCTATAGCGAAACTCCTCACTCTGGAGAAACGATTCTCC  
CCATCCTGTGAGACAAATGGGCAGCGCTGGGAGTTCTCAGCCATGCTGGA  
CGCACGTGGCTCTACCCAGCTCTGTCTGCTGGCTGAGGGAGGGTGGGGG  
AGGCTGGCTGCACAGTGAACCACTTTGGCCGATCCATGCGTTGCTCTG  
GTTTTTCCAGAGCTGCATGCAGGCCGCTCACTTCTTTCTGCTGCTGAA  
ATTCTCTGCTTTCTCCTTTCCCCCACCACAAAAGATGTGAGAACATC  
AAATTCCAGGAGCCCAGATGGTGTGGTGGACGTGGGGAAGAAATACCG  
CAACTATTTCTGCAGGATGTGGTGTGAGAAAGATGGAGAAAGCCTTCA  
GCAAAGTTCCACAGGGTGTGAGAGTCTCTCTCTCTACGTGGGATGGGG  
TTCCCTCCACTTGGGATGGGATTTCTCCAGCTCTCTTGGGGTTCTCCTTC  
CATCTCTGTGCTCCCATGGTTTGCAGCCTGATGATCTTTAGGAAAAGCA  
GCATCCCTCTGTCTCTCTGTGCTTTTCCCTTTGCTTGTCTGGGTTT  
TCCCTATTGTAGCTCCTCCATAGAACTGGGGTTGATGTGGATCTGGATT  
CATTATAAAGGAGGGATGACTGCCTCAAACTCAGCATGGTGCAGATACGC  
AACCAGATGAGGATTTAGGACTGGGGTGAAGGGGGAAAAAAGTGCCAGG  
TGACCCCTAACGACCCCCGCTCTCTGCCCTTCCCTCCAGCTGACATCAC  
GCTGGACCCGGACACCGCTCACCCCTCGCTCAGCCTCTCCCTGGACCGCC  
GCAGCGTTAAGCTGGGAGAACGACGCCAGGAGCTCCCAACAACCCCAA  
CGCTTCGACTCCGATTACTGCGTCTGGGCTCCAGGGTTTCACCACAGG  
CCGTCACTACTGGGAGGTAGAAAGTCGGGGGCAAGAAAGTTGGGCGGTGG  
GGGCTGCACGCGAGACGGCTCGACGCAAGAAAAAACCATGGGGCCTCAT  
CAAAAAGGGGAGATCTGGTGTGTTGGCACCATGGGAAGAAAGTACCAAGC  
GCTGACGGCCATGGAGCAGATGGCTTTGTACCCAGCGAGCGGCCCCGGC  
GCTTCGGTGTCTACTGGACTATGAACGGGGTCACTTTGCTTCTACAAC  
GCTGAGAGCATGACCCACATCCACACCTTCAACGCTTCTTCCACGAGCG  
CATCTTCCCCCTTTTCCGAATCCTGGCTAAGGGCACTCGTATCAAAATCT  
GCACCTGATGGCCCTCCAGCTTCTGATTTTTTTTTTCCCTTTTTCCCCC  
TGCCTCATCCTTTGGGTCCCACTTTGGGACCAGACGCTGCACTTGTGTGTC  
TCGCACCTGCTTGTCTCACAAGGCCTCTTCCCTCCTCTCTCCTGTCCCAGC  
CTCTGTCCACGTCCCAACTCTTCTCCGGGGTCCGATCCCAGGCTGGTTT  
GGTTTGGAGAAGGGATCCAATCTCCTTGTGGAGTTTTTCCCTTCAGCTC  
TTGGTGTATGGGCTCCCTCTGCTTTCCTCCTCGCAGCAGCTTTC  
CAGTGTGCTCTTCCCCGTTTTGTTTAAAGCCTGTGGTTCGAGCTTTCGCTT  
GTTTGGCCTCTTGGATGCAGAGCTCGAGCTGAGGATGCTGGGGTCTGTA  
CATTGTGACACGAGCACTGCTTGTGCCCTTGGCCATTGCTTTCTGAAA

FIGURE 10

SUIITE 35

73/110

FIGURE 10

**SUITE 36**

COSMIDE.txt

74/110

ACTCAGAAACAAGCAGAAAGAGGTTTATTTTACACAGTGTGGAAACTCAGA  
TCCGTTGCCTCACCTGCACCGTGTATTTGCAGACACCCAAAGTGTTCAG  
AGTTTGATGGTTTTTGTCCCTGGAGCCCGAAACGATCTGGCGTTGTCCGA  
GGAGAAGGCGACGCTCAGCACATCCTTGGTGTGGCCAACAAGCGGCGGG  
TGGTGGTTCTCTGCAGGGACACCAGGAGGGTGCACGGGAGGGACAAAG  
CTCAGCAAACCCCATTAATAATTAACCCTCCCCTAAATTGAGGAGAT  
CGTGCTGCAGTGCATAAATTCTTAATGAACACAACCTGATGGAAGCAGGAA  
GGAAGCTAAAACGGAGTCATCTCCACATGGGTTGAGGAGTGGTGGTTCCCT  
TCCCTCCTTCCGAACAGGAACAAAAGGGTGCCAAAGCTTTTGATATAGGG  
TTGGAATAATCATGAGGAGTTTAGGATATAAACTCAGCTTCCGTGGACA  
CACAGCAGCGTAAGTGCTGAACGCTTTTGAGGAGTTGGGGTAGTTCTGCT  
TCCTGAGGAGTTTCTTCTCCTATAGTACTCCCAAAAATCAGAGTGCAAGA  
AGAGCCGGTGCTGCTCCAACCTCACCCCAAACCTCTGTACCCCAAAATCAC  
ACCGAAGGAAAAGCCTGCTTGCTCCAGTCTGTACCCACAGCGATGGTGA  
AGGAAGAACCAAATCCCCCCTGCTGCTCCACCTGCTTCTCTCCCATCAT  
AATTGCAGGACGTGCTCCTCAGATCCCGGAGGATCAGCAGACTGTGTGAGG  
TGTAATCACTGGGAGAGTGAGCTGAGGGAGGAACCGCTTTGGTCTCCCT  
CCAAGCATGATTTACCACCCAACTGAGAGGAACTCACCTCATTTTCACG  
CTGTACCGCACACCTCTCACCCACCCCAACACCCAAACAAAACACAGAGC  
CCAGCTCTGCCCCAAACCCCAACCCCAAGCCCTTTCAGTCCCCAGGACT  
CACGTGGTGAGGTCCACAGCCTCAAGGTGCCATCCCAGGAGCCCGACAG  
CGCAAACCTGCCCATCGGAGGAGATGACCACATCGCTGACAAAGTGCGAGT  
GGCCGCGCAGGGCGCGCTGCGGGATCCCGTAGTTGGTCTCATCTCGGGTC  
AGCTTCCACATGATGATGGTTTTGTCTGGGAAGGGGGAAAGGCAGCGGCC  
TCAGCTCCAACCCCTTCTCACATTCCTCGTCTCACTGGGCTTTATCTCCCT  
CATAGCAATGGGGGGGTTACACAGAAGCACCGCACCCCTTCTCTCAGCC  
CCCCAACCGCCTCCCTACGTCCTCATACACAGCAGCCTCCCCACCCTGCA  
GCTCTCTGTCCCCGAGCCCTGCACCCCATTCATCACCTCCCCTCCCCAT  
GGTCCCCCCCAGCCCCCTCCTTACCCTGACGGTCTCCCCTTATCTCCC  
ACAGTCCCCTCCATAGGCCCCACAGTTCCTTCCCCCCCCCCCCACCCACAG  
TTCCGCCCCCCCCCGCCTCGGACGAGGCCCGAACCCTCAGGCGCGGCCCT  
CACCCCGCGACGCGGAGAGAATCATGTCCGGGAAGTGCAGGGTGGTGGCG  
ATCTGCGTCACCCACCCATTGTGGCCCTTCAGGGTACCGCGGAGGGTCAT  
CTGCTCCGTATGGCGGCGGCGGGGCGGAGGGATGGCGGCGGATTCAATA  
AAGGGCCCGGCGCGGTCCGGTCTACCGCCGCGATGGCCGCCAGCGCGG  
AAGAGAGAAGAGGGAGGTGACTTCCGGCGGAAGCGGAAGTAGCCGCTGGG  
TTGTACGGCAAGAGGGGCAACATGGCGGCGCGCATAGAGAGCAGCTGAA  
TGGGGGAATGGGCTTTGGAGGTGGGGAGGGAAGGTTGTTCTCTGCCGCTG  
CAGGGACACGAGGTGCGGGCAGAGCACCTTCTTAAACATTGCTATTATT  
TAACGTTTTTACATTTAGCATTTTTATTATCCCTGTTGTGCCAGGACGGAG  
AAGAGCAGGGTGTGCAGCCTGTGCTTATCACCTGCAGCTGTCCCTGCACC  
CCACAGCCAACCAAGTTTGTGACGCCTGAGCAGGATCTGACCCAGGAAG  
GCAAACAGAAGGTCTGAGTCCTCCTCCCTTTCTTTTCCCATCCCTCCAC  
GCTGCAGTTTGGGGGCTGTGACCCGTCCGCGTTGCTCAGTGCTCATTCGG  
ATGAGCAGTGTGATGGTGATGTTTACAAAGTTTTTGGCATCCCTGTGGG  
TTCCACCCCGTTTTTGTCTCACCAGCCTTTTTCTATCCGTCTTATCAGC  
AGATCATCCTTGTTATTAGATCTGTCTTTTCCAGTCACGGCTTTGCATT  
TTCACCTTGGTTTTTACCACCTAACATCAAGCCTTTTGTCCCCATCTGATG  
ATATTTCATGCAGATAAATCCGTAAAGCAGGGAAGAATTAAATTCTGGCC  
CTTCTACACCCATTTAGGTTTAGATCTTTGCAGCATTAGCCAAGACGTG  
CTTCCAGAGCCAGGAATAACGTGTCTTGATGTGCCAACACACCTTGAAAT  
CCAGAAAATTGCCCCAAAATAGGCATGACTCAGCAAGCACCGTAGTGGGC  
ATGATTTGTTGGGTGACCCGTGGGTAAAGGAGCCATTTGTTGGACACCA  
CGATGTGCTTTTTACAGCCCTGTGAGCGCAGCGTCTTAAATTGCCCTCC  
AGACATTCCAAATTTGGAGACCTTAATGCCAAAGGTGAAAGGGCGTCA

FIGURE 10

SUITE 37

75/110  
COSMIDE.txt

GCCCTCCGGGATGAAGGAATCTCTGCCGGGGTTTTCCGTTGGATCACAGC  
AGGAGGATTTGCTTTCCTAAAGCATTAGAGTGACGTGGAGAGCCCAAATC  
GGACCCAGTGGCCACATTCTCCCAAGGAAAACCCTTCGGGTGCCCTAC  
GGTTCCTTTTCTAGCATGATAACAACTTCTTTTTCCATCCGCCCATCCCC  
TTTTGGGTTTGGAGGTTGACAAATCCCCACTGAAATTCCTATGTTGCACA  
CATGTCCTTCATTCTTTAAGTAGGAGTTAGCAAAGGTTCCGCATTGACTT  
AATTCAGAGCGAGATCAACAATTTTAGGCATTCTTTATGAACTTCACATT  
GTTTTATGCTGATCAGCAGCAAAAAACATACAGGAATAGGAGTGTGTCT  
GTAGGAGTGCTCTGCATTTTCTTGCTCGTTTGGCTGATTAAGGAAGCTGG  
GAGGAATGTTGTGAAATAATCCCAAGTGATGAGAGACTGTGGGTATGGG  
AGGAGATGCCCTCTGTCTGGTGAGCAGTAGGGACAGAAGACCTGAGCTC  
ATTTTCATATATCTGTATATTAAGGCAATGCTAACCAAGTGCTGTCTGTGTA  
TTTGGGGCCAGGAGTGGCTTCTGCCCGTTGGTGCCCATAAACCAGTGCT  
GCCCCATTTGGGATTGGGGTCTGCTCGCAGACCACATCCACCAACCAACC  
CATGGCTGATAGCAGAGAGGCGACCAGGTCAACCCTCCATATATCTCTGC  
AGAAACCTGTTCTGTCTATACAGGGATCCCCATCCCTCCCCAGCCCTC  
CTTCCATCCTCGGCATTTGGGTGGCTATAATTAGGCTCTGGGAACGTTT  
CCCTGCTGCCAGCACAGCTGTCTGTCTGCAATGATCCTTCCAGCTCTCT  
GCGGACACGCAAAACCCTCCAGCAATCCTAAATACCCATTTCTGCACTCC  
TGGGACAAACTGGGAGCTGCCAAAAATCTCCAGCCCCCACAGACGTGAC  
CATCACAGCACCAAGGAGCAGAGCAAGCGCAACGTGATTACGGTGCGAGT  
CGGGGTAAGCCTTTCTCTTTCTTCCACAGCCCAGGATTTGGGGGATCCT  
ATTGGCTCTATGGGATCTGGGAGATGCAGGAGAAATGTGATCCCTTTGCT  
GTAGCAAAACAACCTTTTAGAGTCCTGCACCTGAATCTGGCAGTACTGGA  
AAGCAGGAGAGGGATTAAGAGTCCTTCTGCATTATCCTGCTCATAGGGAA  
ATACAGCACAGAAATCATTGGGGCTGCTTCTTTGCTTTCTTGGCACAAA  
TTTAGGTCCTCATTACAGCGTTTCTTTGACTGAGACCCCAATAGGATCTA  
CAGGGGTAGAACAAAGCAGACAAAAAGTGATTGATGTTTCTATGCGATT  
TGTTGCCTTTTCCATTGAGATTTCTGCTTTTCTATGGGGCTTTTGGCT  
TTTTACAGCTTTTTTTTATTCACTGTAGTGAATAGAAATTTTAGGGCTT  
TTAGGTCAATTGATGCTGTTATGAACACAGAGATGAACTCATAACACCTTC  
CTGGTGTGGTTTGTCTATGGGATAGAAAGGAGCTCATGGTGTCTGTGGACA  
ACTAACAGAGGTGCCTGAGGGCTGGGGCCTCTTTGTGCCCTTCTGGGGG  
TCAGCAAACTCCTTTTATTAGATATAAATCCCTCATCCACAATTTTAC  
CAGTCTTCCCAATGCAGACCCCAAAAAACATCCCAATGACAAAGTCCAC  
GAAGTGAAGAAAGCAGCAAAAGCCTCCAGCCCCAAATATTTATCCCTT  
ATCCCATTTATTCTATGGGGCAAAGCTATTCTAGGCATCAGGAAGGTGGG  
AGATTCCAGGTCAGTTTGTTCCTAATTGTGATCTTTTAATGATGTTTCTC  
CCATCAGGTGGACATTTGGAAGTGGTTCTGACTGGGAAGAGGACGTGATG  
ATGGCATCAGGTAGAGCTCAGAAAGTGGTATTATCAGCAAAGCAATTTT  
CCAGGTCTGTTTTTCCATTTTTTCCATATTTTTTCTTATTAGGGAA  
GAGGAACGCGGATCTTGGTGAGTGATTTTCTTCTTTTACCTTCAAAAAG  
TCCCTTTCCATGTGTAGAAATGGATATACGTACCCCCCACTGATACCCAT  
TTCCTTTGTTCTGTCTTATATTTATACTTCCCATATTTTGAACACATG  
AAAACAAAGCCACATTAAATAAATTATAACAGTGCAATTTTGGACT  
ATTATTTTCCATAGAAAAGTATTAAATCAGTGCAAGTGCCTCTGGAGG  
TGACTTCTGCAGCACCCAAAGAGAGAGGCGTAGGGCTGAGTGCTCTCTCT  
GTCTCTCTTTTAGAAGAATGGGATGCAAAAATCAGTGAGTGCCCTTTTTT  
CCTCTCCCTTACGGTGAGGTATGGGTGTGGAGGACCTGAATTAATGTGA  
ATTCTCTGTTTTAAGGGAAGCTAACAGAAGATTTTGGTAAGTCGCTTAT  
TTTCTCGATCTGAGTGATATTTCTACACCTTTACCATCAGTGATGACC  
AACGTGTGTATGCATTTCTCTTTATTCCATTTAGAAGAGAGCGACACAGA  
GCTCGGTGAGTGCTTTGGGGTCTTATCAAGGTGGAAAGATGCCCTCTGT  
GCAACAGTGGGGATTGGGAGAAGCCCTTCAGCTCTTCCATTTATCCACAT  
CTGATACCCAGATGGAGTCAGGATGCAGAACTGGAGGAGGAGGCCAAAG

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

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FEUILLE DE REMPLACEMENT (REGLE 26)

SUITE 39

TTGCTCTAGGACGGTCTGAAAAGTGACCAAAATCTGCTTTTACTCATT  
TCTTCTTATTTTTTTGTAGCAAAGTGCGATGCAACGATCAGTAAGTGCTG  
CTGCATGTGGGGGTACCTCCATCTTCGGGTCAATTTCTGCTGTTTCAGCA  
TTGAAAGGACATCAGAATTCCTTAAATCCAACAAAATTTGGGGTCACTCGA  
AGGAATCTTTCAGATATGGGGGAAATCAGAGCCAAATTTTGAGGGGGGG  
AGGGAAAATCTCAGGGGTGTTTCAGAAATCCAATGGGATCTGATGGTATT  
TTCTGCTCTCAGGACTGTTTACAGTGGAACCTCGGTGAGTCCGTTTCCTTT  
TTGTTTTTTTTTTCTAATTATTATTTATTAGTAGTATTATAAATCAATAT  
TACTGTTGCTTATACATATTGTTGTACATTATATACATAATACATACATT  
ATATACAGTATATAGTATACAGTAGTATATAATATTATGTATTATATATA  
TATAATGTATTATAAATGTATATCTAATATATGTCTGTATTAGATAT  
AATGCATATATATTATTGTACTACAGTCATATTATAATACATTACTTAT  
ATCTGCCCTTTTCCACACGTTTCATTGACCTGATTAAAACTAAATCCTA  
AAGGCAGAAGAAGATGAAAACCCCCAAATTAACACCAAATAATTGCAGCT  
ATAGATCATATCTATCAAAGCAAATTTGCCTTCAGTCCACATCACGAAAT  
TAACAATAGAAAGGTTTAAATTTGGAACGTACAAACAATGACAAATAACC  
CCCAATGGCTTTTCTCTTCTTGCAGGAGAGCGTCACACCAAATAGGTAC  
GTGAGGTGTTTGCTACCTTCGTTTGAAGGAAGAAATTGCATTAATAAAA  
CCTCTGTCCAATATGAAGCCGGGGTCAAATTACTCATAAATCACCCTGA  
TTGTCCATGAATTAACAGGGAAAAAAGGCTAACTTGAAAATAACATTT  
TTTTCATCTCTCTTTTAAGGGGAACCTCACTGCAGAAGTTGGTAAGTCTCT  
TTCCCATCAGTTTAAGCAAAAATGGTTCATCAGATATATAAATCCCTT  
ATTTCTGCTTGTTTTAGGGGACTACAACAGGAACTTCGTAAGTGCCTT  
TAACCTTCTCCATTAAGAGTTAAACCTTTCAATATTTTGATGCTTCAAT  
TGCTGAAGCCACCAAAAATGTGTTTTAATTGTAAAGGGGCTGAGCGTCA  
AACCTGAACACTGCCATGTTGGGGGCTGAGATTCTGTTGGGATTGGGTTTT  
CAGTGTGAAAATGCCTCTGGGTTTCTGTGCCTGAGCTCAGGGAAACACGA  
CCAGGGCTTCCAGTAGGAATGAGACCCCAAAATATTTCTACCTGGGGCC  
TTTTCCCATTTGGGAATTTATCTGTAAATCCATATTTCTCCACGTTTGAG  
CGTCACTCATCAAATGTCACAATCTTGGCAATGTTGAGAAGATATATAGA  
TATCTATTTTAATACTGATTAATATGGAGGTGTTTGTGTTGGTCAGTGAT  
GTCATCGGGAAAAGATCTGAGTCATTGAATCCCCATTTCTTTCTCTTTA  
TTTTAAGGGAAACACGACGAGCAACTTGGTAAGGGAATCCCTCCCTGGG  
TTTGTTCTCTTGTTTTCTCTTTGGAGGGGGATTTTTCTATGTCTTCT  
TTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCT  
CTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGT  
TTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATG  
TCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTA  
TGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCT  
TATGTCTTCTTTCTATGTCTTCTTTCTATGTCTTCTTTCTTTCTTTCTTT  
CTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT  
ATCACCTCAAATGAGCCTGAATGTTTGCAGTGAAGGACTGAGCACAGCTG  
GGCACTAATTCATCTTTATTTCTCTTATTTACAGAGGAACGCGATCTG  
AAAATCAGTAAGTGCTGCCCCAAAGCCATAGGGCTATGCTGGGCTTCATC  
CCCACAACATGAATTTTATAAATTAAATAAATAAATAAATAAATAATTTT  
ATATTTTATGTATTTGATATTAGCAGTATTTAAAAAAAAGAATAAATAA  
CTCAAGAATCTTAGGATCAATAGTAACACAATGATGCAACGTGGATACAA  
AAGCAGTAATTCCTATTTCTTTGGGTTTTATCCTTCCAGGGGAACACGA  
AGCAGAGATACGTGAGTGTTATTTTATATACTCTATAATGGAAAACCTTT  
TTCTCTGTAATAATAAAATAGGCTTTATTATTGAGGGGTTTTTTGGCTT  
AACGCAAATGCGAAGTGCTTGAATTTCTACGTATGAAATAGAGGATTTCC  
CATAGAGAAAACTAGCAATTTGGGGCTGGAATAAAAGTTTCATTTCTTG  
CTGAAAAGTGAATGAAAAGGGGGGAAAAGAACATAAAATGAGTTTTT  
TCCCTCATTAATCTGTATGAAATGGGTTGGGTTCTGAATGGTGATGTC  
AACACCTCGTTTTGGGTTTCAGCCCAACATAATATGTGTCTGTCCTTTATT

FIGURE 10

SUIE 40

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TCTGTATCACTGGTGTTAAAGAGAGCTGTTTTGAACTAATATCTCTTTTT  
TAATTACTTTTTCTTTTTCTTTTTCTTTCTTTTTCTCCCGTTTCTCTC  
TGTTTTGCTTTAAGGGCGCCTCACTGAGCTGCTCGGTAAGTGCATTTCTC  
TCCTTGCACTGTCAATCCAGCAACAACCAAAGCCTATTTGGGGGGGA  
AGGAGGGGATAAAACACAATAATGATGAAATCAGTGCTTTGGAAAGGGTG  
CAATTATTATTTCTCTGCAAATGAATACTTCTTTTTCCCTTTTGTTCG  
AGAGGACCGCGATTCCGATGTCCGTAAGTCCTTTTGTTCGCGGAGCT  
GTGAATCCTCCAATGGGAAATGCAGAATTTAGAGTCTGCCCCAAAAATG  
ACCTTTTTGAGGCTACAAGGGATGGGAAAATAAGGAGAAATGTCTTATT  
TATTGATCTCCTTGTATGTGCAAACTGGGTGACTCTTCTCTGCCGAA  
CACGTTAGAAATAAGAACACAAAATGGGAGGAAATGGTATTTATTCATAT  
CTGTTGTTTTCTGTTAATTTTTAGGAGAACAGGACATCCTCATTAGTA  
AGTGGCACTTTGGATTGATAAGAAATGCAGCTCCTGGGGACGTTTGGGTG  
CTGCGATTGCTGGCACTGCTGGGGCTTTGTGTTGTGGTGAAGTGAATT  
ACTTCAAAAAGAAGAGAAGAATGGAATTATCTGGAGAAAAAGGGGAATAA  
TGGAAGTGTGTTGGGAAAAGAAGGAGGAATAGAATGGAATATTGGGGAAA  
AAAGTGAATAGAATGGAATTATTTCAAAAAAATGGAATGAAATTTAGG  
GAGGGGGAAGGGGAAGTGAATGGAATTATTTGGGGGAGAAAAAGGGGAA  
AATTGAATGACTGGGGGGGGAATGGGGAAATAGGATGGGAGTATTTTAA  
AATACAGAATTGTGAAGTTTCAGCCCATCTCAGAGAGTTTGGTATCCTC  
GAGTTCCTTTCTGCAACCCATTGAGCATCCTTGGGATGACACCAAATTC  
TGTTTTCTCTTTTCAAGGGAACCTGTGAGAAGAGCTCGGTGAGTTATTT  
CCAATTCTTACATACAAAACCTGATTCTGGATATCTTTTTGTGTGTTTT  
CTGCTTTGCCTCTTTGTGTTTTAAGAGGCAACTGCAGAAGGAATGGCACA  
AAGGGTGCAGAGGATCTTTGGGATAAATAACAGGGAAAACAGGGATGGGA  
TAGCAATGAGTTGGTGAATAATCTATGGCACAAGGTGACGGCGTGTT  
TCACATTTTGCTTTTTCTCTCCTTTTAGAGGAATTAAGGGGTGCGGAAG  
TTGGTAAGTGAGATTCCTTTCCCTCTTCTCCCCAAAAGGATAAGGGGTAA  
TTTGGATTCTGATCTCTTTTCTCCTTTTTGTTCTAGAGGAGAGTGTT  
CTGGAGAGGGGTGAGTATCATTCTTTCTACTGCTGCTTTGACTGAAG  
GAATCCCCCATAAGCATGCTGGTGGGATGGGAATTCTACATCTGATACAC  
AATTATTATCATTCTTTCATTTTTTATACACAGAAATAGATAATTTTTTT  
CCTTTCTTTTCTTTTTCCCCCTTTTTTAGAGGAACATGATGCCAGAATT  
GGTACGTGTCCATCTCCCCCTGCTTTTGTGGTGTCTTCAAGAAGGCCAAT  
GGGGTCATTTGGGATTGTTTGGGTGAGGATTGGGTTCTTGATTGAATTT  
GGGGGAGGATTGAGGTGCCCCAACACATCAGGTCCCATCTCATGTTT  
TCCTATGGGCTTGATCCTTCTGTTGGATACCTAAGAATACCTGAAATCC  
ATAATATGCCATTAGAAGTAACACATCCATCAATGATATATCCATAGAAT  
ACAAGAGAACGGTCTACATTTACTTCAGATCCCATTTTCAAGTTAACCAT  
GAAAAAATAACCAAAGACTGAATGTCACCATTGAGGGATCCCGTGTGTA  
AAATCATGACTTCTGCTTTAATTATAAGAAAAATGAAATTCAGTGTTTTT  
ATTCTCTTTTAAGATGAACCTCTCAACAGAAGTTGGTGAGTATTTTCTGC  
CCTCCAGCAAAACCAAAGCATGCAGTTTGCAGTCTGTTTTGGATATATAT  
TGACGTGGATATATAACCTGTATGTTATAACACCTCTGGTTTCCTTTTC  
TCCTTCTTTTCTCAGAAAAACGAGAGAGAAGAATTGGTGAGTATCAAAC  
TTCCCCCAGAAGTGGACTTTGGTGTGTTGGGAAGATCCATACCACCAG  
TTGGTGCCAACTTAATGGAATCCTTTGTTTTTCTTTATGTTTTCAGA  
TGAATCACTGCAGAGCTCGGTAAGTCGTGATTATAACTATAACGAGTT  
ATAATGCTATTGTTATATATAATATACATATTATATATTGTTGCTATAAT  
TCATAATAGAGCAACAATCACAAGGCACAGAAATATGGGTTTGCTTTGA  
GAGCCAAACCTTAGGAAGTGATAACACAATGGGAAGAGGACAATGACCAT  
TTCTGTGTTCTCTTTTTCAGAGCACTACAAGGCAAAAGCAAGTGAGTGT  
CTCCTTCTCATCTTCAGCACGTGAGAGATTTTGGGGGCTTTTGGGACGG  
CTATGGGGATTACACATAATAAACAGAAGATGAGAAGACAGTTTGTGA  
ACTTGAATTCAACTGGTTTCAATTTGCTCAATTTAGAGTATTAATAATC

FIGURE 10

SUITE 41

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COSMIDE.txt

TCCCCAGTACCCAATTATACAATGGGATTAATTACAGCCTGCCAGGAAA  
GGAGCACTGAATTTTTTCTGCGTCCATCCAGCATGAAGTCCATCAGACT  
TAAGCTTACAGCTTAAAGAATGGTTCATTTTTTTCATTTAACCCCTCGT  
AAGTTAAAGATGGACTTCAGCATCACAGAAGTAGCCCAGAAATAGTCAA  
AAAATGGGTCATGAATTTCCAGAGCACCCCCCACACTTTCCTTGGTGAA  
TAGGAAAACAAATATTAATACTAATTAATTGGTTTTTTTTTCTTTTTAGG  
AAGATGTTTTGAGGAACACAGTAAGTGCCCTTTTCTCCCTCTTTAAGCA  
TCACTTTTCACTTTAAGTCTGCATCACAGTTAATAATCCATCTCCTTATT  
ATGCATTTTTAGGGAGAGGCGAAGAAAAGTTGGGTAAAGTCATTTGGTTAA  
TTGGGTTTTCTGCTTGCAGACCCCATCCAGGAGCTCATGTCCTCCTCTTAG  
TGCTGCACTGTAGAAATATCCAGGTTAGACGTGTAGGTAGGAAATACTG  
GACCTGCGTGGAGGTATTGCAGACCCCATTTATGTGTAGGGGAAGCAGAA  
CATCAAATATTGAGCCTTGAGCTCCACGAAGACAAGCCACCTCTTAGA  
TTTCAAGCGAAGTCGAGCTGAATAGATTTAATTCTTTCTTTCCCATAGTA  
AATGTGACTCTGGACCCAGAGACGGCCACCTCGCCTCGTCTCTCCAA  
GGACCAGAAGAGCGTCCGATGGGAATACAGCCTGCAGGAATCCCCGACG  
GCCCCGAGCGCTTCGACGCCGATCCCTGCGTGCTGGGTGTGAAACCTTC  
ACCTCTGGGAGGCACTGCTGGGTGGTGGATCTCACAGAAGGGCAGTACTG  
CGCCGTTGGGGTCAGCAGGGAGTCCCTGCCCAGGAAAGGAGCCGTCACTG  
TTAACCTGATGAAGGCATCTGGGCTGTGCAGCAATGGGGGTTCAAGAAC  
AGAGCCCTCACCTCCCCCTCCGACCCCACTGAACCTTCCACGGGTTCCCAA  
AAAGATCCGCATCTCTCTGGACTACGAATGGGGCGAGGTGGCGTTTTTG  
ATGTGGAGAACCAAATGCCATCTTCACTTTTCTCTGACCTCCTTTGGT  
GGGGAGCGGCTCCGGCCGTGGTTCTGGGTGGAGCTGGGCTCCCTCTCACT  
GCCAGATAACCCCGGAATCCCTGGAGGTGCTGTGGAGGTGCCTTACAGC  
AGCTCTTCCAGACCGGGGTGGAATACTCTCAGGAAAAGCAGCATTAAAA  
CCTCATTCTCCCTCTTCCCAGTCAACCATTGTCATGCAAAAGAAAGGAAA  
CCCATCCTCAATGTCATCAGCATCCTCCGTGTGTCATGTCCTGGTGGCCCC  
CATTGATGTATGGGGTGGCTCCTGTTGGTGTCTGGTGGCCCCCTATTGACG  
TATGAGGTGGCCCCATTGACGTGAGGTGGCCCCCATTGACGTGAGGTGG  
CCCCTATTGACATATGGGGTGGCTCCTGTTGATGTCTGGTGGCCCCCAT  
GACATGAGGTGGTCCCCATGACCAGCCCTACCCTGGATCCAATGCCTCC  
TGATTGCAGTTCCAACTCTAGGGACGTTAAACGACCCACAGAGAGGATG  
GGGTCTCTTTGGTCTGATGGAGAGAGGTTGGCACCAGGGTAAGTCGCTG  
CCTACATCACCCTGGTGTCTTGTCTCAGCAGCTGGTGTAAATTTCTGCC  
ATCTGGGCTATTTCTGTAGAAAGCAAAGAAGCTCTGCTGGTGGGCAGCTC  
ATCTCCCAGTGTGAAAAGCAAATGCAACGCATGCACCTGCTATCCAT  
GTGGCCATCCCTCTCCATCAGCTGTTGAAGGAGAAATCTGCACTCAGAAG  
AGATTGAATTGGGCTCAGATCTGGCTTGGGAAGATGATGATTCCAACCAG  
AGTCCAGGAGACTTTGGGAATGCATGAATCCTATAGGAAAATGGATAAC  
CCTTCATCCAAGAGCAAGCTGGCATGATGCTCTGGGGTGAACCCATAA  
TGCCACCTGGTTTTAAGGTTTGGGGTGGCTTACAATGTGCAGCTCTGCTT  
CCGGCGAGGCACTGGGAGCCCTAAACCCATGGAGAGGTCAAACCACTGCT  
GGAGGTCAATTGTGGGCCAGCTGCAATGGGAGGTAGGCAATTATGGACAT  
CGCTGAAGCCACCCACGCTCTGGGGAACCTGGGTTTTACCTTTCACTG  
CACTTTAATGGGATTTCTCATCAATGTCTGCATGTTCTTGGCCACCTGTT  
TAAAAATATAATAATAATAATAATCTTTTGGCCCACTGCGGGATGAGC  
AGCTGGTGGTTCAGCTCACAATAAACACACTTGAGACTCCCTGGAGA  
ATTCGCTTTCTTTTGCAGCTGGTTCCATGTGGGGCTGTTACGCCCCCTCT  
GCAGCTCATAGGCTTTTCTTACAGCCTCTGCTCCACCTATTGCTGAAAA  
GGGGGAAATTTGAGATGGATCCCATTTTGTGAACATCTCCACCTGTGGG  
TAATGCTCAGACCTCTCAGCCCTGTGGGTTTAAATTTCTCTTTCTGCAGCT  
TAATGGGTTGGGGATGTTCACTACTGCAATAATAGTGATGGGATAGGGG  
AGGCAGGAGAGGATCCAAGCAGGGGAAAGGGGAGGGGAAGGACATACTGT  
GTGTGCTG

FIGURE 10

SUITE 42

COSMIDE.txt

FIGURE 10

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SUITE 43

TGTGGACCACAGTATTCTTACCACATAGGATTTGCTTTGTACTGAAGGTT  
GGGGGGTTTTTTTGGTCGTTTGAATAGGAGTTGTATACACTATTGGAAAAC  
AATTTGCATTAACTCACACTATCAATCATTCTTAGGCCTAAGAGCATCTG  
TTTTTTTAGGACCAAATCCACAGATCCACATAAAATCCTGCACAGATAT  
CCATGATAAACATGGTGGGAACTGAAGCAGGCAGATGTGGGACATGACAT  
CCAACCTTCTGTTTCATCCCCAGATCTTTTTCTATCTGAGCTGGAGAAGGA  
GGAGGGAGCATCTGTAGGAGAAGAGGGAAAAGGTGAGTCCTTAAAGCATT  
TTCCTTTTGTCCATTGGTCATTTTTTTAGCCAAAATACTGCGTCAGAGC  
ATCTGGAAAATGATGGTTTTTGAGCTCATTCTGGTTTTCTAAAGGTGATA  
TAAAGAAGCTTTCTTATATTTTTCAGCAAAGTTTTCTGAGCTGGAAAATAT  
GGAGACATCGCTGATCCCAAAGTAGATTTGGGGTGCTGTTCCAGCTTTAG  
GGTGATGCTCACCCATTTCTTCTCCATCCCCAACAGCGTTTGTACCCTG  
GACCCCACTGCCACTGCAGGGCTCGTCCTGTCCCGGGACCGACGTGG  
GGTGAGATGGATGGATATGGGGCACAACATGTCCCCTTGCCCCAACGCT  
TCGATGTCTCCTGCTGTGTGCTGGGCTGTCGAGGCTTCACCTCAGGGTGG  
CACTTTTGGGATGTGGAGGTGATGGGTGGTGCCACGTGGGCACTCGGGGT  
GGCAGCAGCTCTGTGCCCAGGAAGGGTTGGCTCACTTTCCACCCCGATT  
ATGGGATTTGGCTATGGGATGCTGTAGGAACAGCTTCCGAGCTTTCACA  
TCTCCCCATCC

SUITE 44

WO 99/27132

PCT/FR98/02501

82/110  
D12FOR.txt

GGGGGGCGATATGGGTGGTGGGACATGAGGGGGCCGGGGGGGGTTCGGGTC  
TCACCCGCCAGCAGCAGCCGCAGCCCCGAGCCATTGCTCTCCGCTGCTT  
TCGCTTTTCGGCTCCGCTGTGGCCCCACCCCTCCGTCACTTCGTCAATAT  
TAATTTTAAATCCCTGAAACCCATTAAAAAAGGGTCGGAGAGGGGAAAAC  
TCATTTCAGGAACAGTGTTGGAAGAGGGGACATGGGTGGGACAACCCGGCT  
TTCCCCACAGGCCGACCTAAACACAGCCACTGCCACCCACCCCGGATCCA  
TGGGTGACGTAAGGATGAGGTTCCAGCACATATTGGACCCTTCTGCGTTT  
GCATGG

FIGURE 10  

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SUITE 45

83/110  
E1REV.txt

GTGGGGGGCAGCGTCCGCGCTGACCTCGTCTCGCTGTGTTTCAGGGCGCC  
CCGTGCGCGCGCTCCAGGTAACGTCCCGTCCCATTCCCGTCCCGTTC  
CCGTTCCCGTTCGCGCTGCGCGGAGCGGCCCCGATCCCGGCGCGGGCT  
CAGCTCTGCCCCGTCTCCCGCAGGGATGCTGAATTAGCTGCTGCCCCGCC  
GAGCCGCTGCACCCGCACCCCCGCTCTCCCGGCCGTGCGCTCGGCTCTC  
CCTCGGGCTGCCACCGCGTCCGTTGGAGATGTCGCCACGATGCACGCTTC  
GTCCCCATCCTAATAAACGCGCTGACTTTGACCCGCTGTTGCTGCCCCG  
TGAATCATTGGGGACTTCCGTCGCGTGGGAGGAGGGGAGGGAAGTGAAA  
GCTTCGTGGAGAAGTAAACCCAGCACCCCTATGGGTCCACGGGACGTGGA  
TTGGTGGGGATGGGGTGGGATTGGACTCTTGGTGGTCATTTCCACCCATA  
GGGAGCTCGCGGCCACCCAGTGGTCCTCATATAGACTCCATGGTCACACC  
ACTGTACCTTTTGGTCAACCCATGATCCCTGTGTTACCCTCCGGGGTCC  
CTCAGTGGTTACCCACGTTCCCGCAGAGGCTCCTCCTGTGCGCTTCATC  
ATCTCACCCCATTTGACCACATACCCCCCTCCCCCTATGGATAACCCAAAG  
CCATCACCAAGTGGTGTGGGATGCAAACACGGGGCCCCGGACCTGTCCCT  
ACAAGCACAGGGTGGTGACACAGCCCAGACAGTGTGCTGTGTCATTTGT  
CACCAGGCAGAGGACACACAGCCACAGCCTGGCTCAACTCGAATAATATT  
TTCTTTATTTACATGTTAAAGAATCGAAAGGTGGAAACATACAGTAAGA  
TGAAACACGGCTCTAAGGGTCTAACAGTGGGGCAGGAGGGTGGGGGGGA  
GGAAAAAAGAAAAAGGGAAAGAAAAACCAAAACAAGTAGAAAAAA  
ATGATACAGTCAACGTAAAAAGGGGTGGCCCTCCCTCCCCAGTGGGAA  
CATGCGGCGCTGCGTGCCGGGGGGTTTTATGTACAGGGGCGGGCAGCTC  
CAATAAATTAACCTCCAATAACAATGAGGGGGGAAGGGGGGGTGCAGA  
GCCCCCTCGCTGGGTGGTTTCTTCTTTAAATGCTTTTTTTTTTTTTGT  
AATTTTTTTAATTTTTTTTTTTTTTAATTTTTCTTAAAAACCCAAACCTT  
TTCTCCCCCCCCCTTTTTTTTTTTTTTTGGAAAAATCCCACGAGTCAG  
GAGGAAAAAAGAAAAAGCCAACCTAACACAACAAACAGTAAACCT  
GCTGGGGGGCACCGCGACCCCCCTTGTCGACCCACAGCCCCACACT  
GCCCTGGGGACGCTCGGGGGCTCCGGTCACACCGGGACCCCCAGCTGAG  
TCCATGGGGCGTCCCTGGGCTGCTGGGGGGCTCTCGGTCTGCTCCATGC  
CGGCCCGGTCTGTCAGAGCCGCTCGGGATGCTGCCCCATGTGGTGTGTG  
GGGTTTAAACCGAATCCGAGTCGCTGGTGTCCGAGGACGAGGAGCTGGAA  
CTGGAGCTGCTGGAGTCGGAGCTGGAGCTGGAGGCGCTGAGCCGTGAAAC  
AGCCACCTGCTGTGCTGACTCGGGCTTCTCGTTGGCTGCAATGGGACAAC  
ACTGCGCTCAGCATCACACAGATCACACCCCAATCCCCTCCAGACCCC  
ACACTCACCTTTTTTGGGGGTTTCTTGGCTGAGTTGAGCTGCCCGCTGA  
CGTCTGCAGCCGCTTCTCCAGCTCCCGCTTCTTCTCCAGCGCCAGTTCT  
TCTTTCGTCTTCCCCACCGGCTTCTTCATGGCTGTGAAATTCAGGTTTCAG  
CCCCACACCATCCCACCTCCACCCAGGGCCGCCCCCTGAACGCAGCCCC  
CCACTCACTCTCGCTATAGGGTTTGCGGGGTTTCTTCCGACGGCAGGACA  
GCACGTAGCGCTCCAGCTCACGCAGTGTGGAGGGTTTGAGGGTCTCGAAG  
TCGATCTCGATCTCCTCGGGGTTGGAATCACGCAGTGAAGGCTCCCGGGA  
CTGGATGATGTGCACACACGGCCCCAGCTTCTCCCCGGGCAGTTTGTGA  
TGTCCAGGCTCAACTGCCTCTTCTCATCGTACGTATCGGTTTGTCTCTC  
TCTTCTCTTCCGAATCGTAGAGCGTGGGCGGAGGCGGCAGCGCGCTTT  
TGCTGCTTTCTTTGAGTTCTTGCAGGAAGCAAAGCACCATCAGGAAATG  
AACCTCAGGAATCACCCACAGCTGACCATCATCCCCCAAAAAACAGCCT  
AGACTCACTTGGAGCTGCCCCACCGCTCCCCCGCCGCCACCTTCTTG  
GCTTTGCGGAGCTGTGCCTGACGCGCCCGGCTCTTTCATCTCCTCCTCG  
CCCTTTGTGCTTCTCCGATTTCTTCTTTTTTCTTTTTCTCCCGCTTCTTT  
TGGGTTTGGAAACGGGGCCCTGTGAGAGGGCAGCCAGCTGCTCGTGACG  
GCCGCGAGCTGTGGGGGGAGACAGGGGGTGAAGCGGGCATGGGGAGCAGG  
CACAGGCAGCAGCACCGGCCAGCTCCGGCCCTCACCTGCTCCTGCAGCT  
CTGCCAGGCGGTTGGCACGTTCTTCTCCGAGTCAGAGCTCTCCTCGCTG  
TCTGATGAGCT

FIGURE 10

SUITE 46



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E1REV.txt

TTCATCTTCATCATCCTCATCGCTGGAGGATTCTCGGAGGAGGATTTGG  
AGAGGGCTCCAAGCAGTGGGGCAGACACTGAGGGTGGGCTGGCGTCTGC  
GGCTCATCAGGCATCTTGGCGTAGCTGAACTCAAAGACATCCTGAGAGAG  
AGGACACAGAGGGGTAAGCTGACTGGGCTGGGGGTTACGGGGCTGCTGGG  
TGACCCACCCACCTGCAGCTTGCGGGCCATGGCCACCACATCGTGGTGC  
GGAGGGTTGTATTTGTAGCAGTTGGAGAACATTAACCGGACATCAGCGGC  
AAACTCCTGTGCGTCATGGTAGTCCCGGTTCTCCATCTTCCGCTGTGGGA  
AGGGAAGGCGTGAGCAGACCTCAAAGCCACCCCCACAAAGCCCCCATGA  
GGCTGTGCCAAGGCCACGGAGTCCCCAAGCGAACCTTGATGGTGCTGAG  
GTCCATGGGGTGTGTGATGATCTCGTGGTAATCGTGCAGCCCCAGCGCCG  
AGGCATCGACCGGCTTGTAGAAGGGCCATGCGTAGGCAGCGTGCTTCTTG  
GAGAGCAGCTCCTTCAGAATCCCATTGCAGTATTTGAGCTGCTCCGACAA  
TTTGCCCTTTTTGGAGGTCTGATGCTGCTGGGAATCCGGCAAGTCCTTCT  
TGGGGGGTTTTGATGGGGCGGCCGCTCTCACGCCGTGCGGGAATTTTGGCC  
GCCTTGGCCTCCAGCAGCGTGGCTGACGGGGAGGATTACCGCTGGTGGC  
TATGATGGCGGTGGTGGTAGGGGTGGTGGTGTCTGCTTTCCGCTTCACAC  
CCTTTTTCTACCAAAATACAGAAAGGTTGATGAATGGGAGGCCAGCACA  
GCCACAGAGCCTCCTCCCGTGAGCGAAGAGCTCCCATCTCCACCTTGG  
CCACGGGTTGGGTGGGCGCAGGCGCAGTCAGCACAGCCGGGGCAGTGGAG  
TGCAGCGACTTGAGGAGCGGAGCGGAGATGACGGACGGGTGGGGAATGTT  
GACAATGGTGGTGGCGATGTGCGGGGCTTGGGGTGTACACAGCGGTGTGGG  
ACACAGAGGAGACAGCTGGCACTTGCTGAGCCGCTGTGAGACCTGCCAGG  
AGCGCTGCGGACAGGCAGAACCCCATAGCACCAAGGTACCTTCAGTGC  
TCTACCTGAAAGCGCAACCCAAAGAACCCAGGTACCTGCTGCCCGCGAC  
GCTCCCTTCTTGTGGCTGTTTTTGGCCACTGGGACCAGATCTCCTGCTC  
TTCTGGTGGCATTTTGGGCCACCTTCTGCAGGAAGATCTTCTCCAGGGTTT  
GGGCCATCAGCACAAATGTCATCTGTGGGCTACAGGGACAACCGAAACGTC  
ACAGGATGCAGAGATGGCATCAAAGGCCTCAAAGCATCCATGCTGCAGTC  
CTCACCTTGTTATAGATATAGCAGTTTGTGAACATGGTGTGAAGTCTTG  
CATGCACTCAGCTGCCCCCAGTAGTAGTTGTTCTCCAAGCGCCGTTTGA  
TCGTCCCCATGTCCATGGGCTGCTTGATGATCTTGTGGTAATCCTGCATA  
GGGGATGGACAGTCAGCGCCGTGTGGTAACCACACTGCACCCCTCCAG  
CCCCAGAAGCAGTGGTTTTGGGGTTTTTAGGAGCTCAACATCCCCAAAGT  
ATCAGGACGTTGACACGCACACAGATCCGCTCTCGCACCATGCATCAAAA  
GCAGGGCAAAAGGTTGCAAAGGGATGGAAAAACACCTCCGGGTCTGGTCC  
CCGCCGAGAGTGCCACCGTGTCTGTGTAGGGGACCTTCAGGTGCTCT  
TGTGGGTGCTTACGCTATAGGGACAGCCAAAACACTGCTGTCCACAGCA  
TGAGGTGCAATGGGGGCCACTAATGCTAAAGTAAGAGCAAACCTATGTGG  
AATTTACCTCTGGGCTTTAAATCCTTGGGCGCCACAGGTACACAGGGGGC  
TGGCGTTAATATTGGGGTCACAAGATGTCTTCTACAAATTTCATGGATGG  
GAATCTGCAAAACGCATTTCAGGGCACAAGAGATTAGGTGAGGAAACATCC  
GGGTTCCCTCTAGAGCAGCTGCGTCACCTCACCCATAACCGTGCGGTGGC  
ACTGGGAGGGGACAGCAGCTCTGAGGACATCAGGTACCTACTGGGGGGG  
CTTCAGAGCCTGTGGAGTTGGGATTATGCCCTAAGAGAGGGCGAGGCCA  
GCACAGCCCAGGCACCTGCAGCTGCATCTCTGTGGTGGAGCCCATAGAGG  
GGACAATGCTGTCCCTGTGGCACTCTCAGGCTGGGGACCACGGCTCGGGG  
TGGCCCTCAGCACCCAGGGGACAAGTCTGGGGACACACAGCCATGCTGGG  
GGACCCACAGGAGGGGACACGTTACCGGCAGACCCAGCTTGACGGCGTCCG  
ACGGGCTGACGGAAAGGCCAAGCGAACTGGTGCTTCCACAGGGCTTTTCAT  
CACCACCTTGTGCAAGTACTGCAGCTGGTTGGTGACCCGGCCGGGCTTTT  
TGGGGTTTCGAGACCTCTGGCGGAGGGGGGTTTCGCCTGGGGGGTCTGTAGG  
GCCGGCACCGAGGCCATGGTGGGGCTCTCGAAGCCCTCGTAAAGCAGCGA  
GGGTTTGGGATGCGTTTGGCCGGGGTGGATTCCGTGCGCAAACCCATAA  
GCCCGGCATTTCCCTCCCCAGAATCCTGCAAGGGAGCAAAGACAACAT  
CAGCAAGGATGGGGCCAGCGTTCCACCACCAAGGTGCACAAGAACAGCTC

FIGURE 10

SUITE 47

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E1REV.txt

AAAAAAGGCCAAAAAAGTAATCAAAAAAGGAAGGTTGGAGCAAACAAA  
GAGTCAGTGCAGGGGGTGACATCAGGGCCCAGCAGTTTCACCACCTCGGG  
GTACGACAGCCTGCACTACAGCATGACAAGGCAGCACCCAAACACTGTGG  
CCCTCAGCTGGATACACAACAGTGGGCTCCAAATGTCTGGGACGGGGGC  
AGAATTATTTAAGTGGGGAAAATGAGGATTTAAGCAGCTGGGAGAGGTGG  
GATGTCTGCAGCGTGAGGAGAATTTGTCCCGGGAAAATACGGTGAATGT  
CGAGCACTGGGGCTGCTTTCTCAGGCAGCTCCAGGGTGTTCCCATCCT  
GCCAAGGACGTGGTGGGAATGACAAGGAAGGAAGGTGACAGAAGGACACA  
GCGGCCCCAGTAGTGGCGGTACAGGGTGGGAGGACACGGTGAGACCCCTC  
AGCATGGTGACAGTGTCCCCGAAAGCAGCTCAGTCAGCAGAGGTGGCAGC  
AGGGCCCTAAGGGCCCTTGTGATGCTGACCCCAAGGACCAGGGGTATGAG  
GAGTGGATAAATGGGGGTGGCCAGACAGGATCCATGGGAAAACAGGGCT  
GCCAGGTTCCCTGTAGGATCTGTGTCCCTGCATCCCTGACAGAATTCACA  
TGGACCACGGGGCTGCCGAGTCCCAACATCCCTGAAGGACCCACAGAAAT  
GGGAAGTGGATAAATGGGAACAAGCAGCAGATCAATGGGACTCAGTGACC  
CCAAACTCAGAGCTCTGTGACAGAAAAGCCCCATAACTCTGGTGGACATC  
CACACTGCACCCTAATCCCTGGGCAATGAAGGGATAGCAGCAGGGAACCA  
CTGTGTCCCTGTATCTCTGACCCCAAAGAATCCATGGAGATGGGGAATGG  
ATAAATAGGGATGGCTCTGTAGAATCCGGGTCCCATTCCCCTCAAATAAT  
CCATGGGAATGGCACTGTTGGATGCATGGCCTTGAGTCCCTGTCCCTAA  
AATCTGTAGGAATGACTCTGTGCTATGCACCTCCCGTGTCCCTGTTAGG  
ATCCATGGGGACAGCAGGCTGCCAGGTCCCCTGTATGATCCACAGCCCTA  
AAAGCAGCTTGGTCAACAAATGGGAGGGAACAGCGGGTCCCTAAAGAGCG  
CCAGGTGCGCATGTCCCTGTCCCAAGGACCCACAGGTACAAGGAACGA  
ATAAACAGAGACAAGGAGCACTCAGTGGGATACAACCTGATGTCAGGTGCA  
GAGCCTTTGAACACAGAAGCCCCATCTCCCATAGGATTCAGGTCCCAT  
GCCCCTGTTGGAACCATGGGGACAGGGAGGCTGATGGATTCCCTGCAGGA  
CTGAGTTCCTGTGTCCCTGACCCCGAAGAATCGATGGGGACAGAGAGTAG  
ATAAACAGCGATAGCCCTATAAGATCCAGGTCCCGCGCTCCCTGTCAGGA  
TCCGTGGGGACCGTGGGGCTGCCAGGTCCCCACGTCCCCGTCCCCAAGCA  
ATCGATCCACGGGGATGAGGAACACATAAACGAGGACAACCGGCATACAA  
ACGAGATCCAACCGGGCCCCGGGTGGAGCACCGGGACGCGGCAGCCCCATA  
CCGCCGTCCCCGACGAACGCCATCCCCGGTTCATAACTGCCAACACCCC  
ACAGCCCCCCCCCGCCCCCATTCCTGCCCTCATCACCTACTTGCTCTGG  
GGATTACATTCTGCAGCATGCCGGCGGTGCGTGCCCGGCCCTGGCTCC  
CGGCTTCTCTCCACCTCCTCCTCCCGCCGCGCCTCCTCCGACGTCC  
CCCCCACTTTGCCACCGAGCAGCGCCGTTAAGGCAGCGGCCCTCGGCC  
GGGCATGAGGCGGCGGCTCCGGCCGGGCCCCGCGCGCGCCCTCACATCA  
GCGGAGAAAATGGCGGCGGGGCTGGATGGAGAGGGGGACCTTCCTGCT  
CTCCGCTGCGCACAGAACC CGCGGACGCCCGCATATAGAGCCGGGAA  
AGCCGGTAGGAACCGGATAGATCCTCGGAAGGACGGTGTGAGCGGATGG  
AAGGCGGACAGAGGGCGGATGGAGGCGGATGGTTCAGCGGGAGGGCTCCA  
TCTTGCTCGTAGGCCCCGAAGAGGAATCGGTGCCGGCGGCGCAGGCAG  
GGGTGCTACGGAGGCGGGGAGGGTCCGGTGGAGCGTCCGGGAGCGCG  
AAGGCGGGGGCTGGGCCGCGGTTGGAGGATGGAGGCGGATGGGGGCG  
CCCCCAGCGCGCGCGGACCCGACCCGACCGTCCCTTCGTCCCCACGA  
AATGGCGCGGCTCGGCCTGCCCCCGGCCCTTATATAGACACCACCTG  
GGTGCTGATTGGTGGGTGGACGCGCTGACGTGAGCCACCCGCTTGACCC  
GCCCTGCCGCTGCCTCATTGGACGGCGGTGCTCACC GCGCAGCGCTCCTC  
TTGGCCGCCCCGACGCCACTCACC GCGCGCTCCCCCCCCGCCCTTCC  
GCCCGGTACTGCGACGGTCAATTGGTCGGTGCTGCCATTCGCGGCGCGCG  
ATTGGCCACCAAGGATCACGTGAGGGCGGCGCTGTTGGCTGTTGTTGTCG  
CGCGCGAAGGTGCAGAGGGAGGGGAGGGCTAAGGCGGGCGTCGCCATTT  
TGTGTGGCGGCGGCAACGGGCGGGCGTCCCGGGGTTTCGGACCTCC  
GCCCAAAGGCTCCTCAGGGGGTTCAGCAGACCCCACTCAGTCCCTACGGG

FIGURE 10

SUITE 48

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E1REV.txt

GCTCGTGAGGCTCTCCAGCCGACAGCGGCCATCGGGCAGCGGAGCCGCG  
GCGGTCCGCGAGCCGCGGGCTGAGCTGTGGTGAGGTAGTGAGCTGGGTCC  
CGGGGATCCTGAAGGCTCCTGAGGTAATCGCGGCCCTCAGCGCGGTCCCG  
GGGCTTCAGTGCCACCCACGGTGGTACTGGGGCCCTCAGACCGTCCCC  
TCCCCACTGCCACGGCGATCCGGAGGGGGGGGGTCCGAGGCCGCCCGT  
GTCTATTCCGAGGTGCTCTGTGCTCTTCTTCCCCACGGCAATTCTGGAGG  
GCTCACAGCTACTCCAGAGCAGCCCCATAACCGTCTGGGGGCCTACTA  
CCACCCTACAGCAACTCAGAGCCTCCCCCACCACCCCAAAAAACAATC  
CTGGAATCCCCAAGGCCATCCACACCAACGCTGAAGGTCTCAAAGCCCC  
CCCTCCCCACACACACCGGTTCTAGGGTCTCAGAACCACCCACAGCA  
ATCCTGGGACGTTCCACAGCCCCTCCGTAGTAATCTTTTAGTTTCTCAAG  
GCCAACCCGTAGCAGCGGGGGCCTCCGCTGCCCTCCCCCTCGTGGCAATCCT  
GGGGGGCTCAGTGCCACCTCACAGGAATTTGCGGTGCTCAGAACCTCTG  
CAAAGCAATCCTGGGGTCTCGAGGCCACCCACACCGATCTCAGGGTGC  
TCAATGCCACCCACAGCTGCCCCGGGGCCGTACAATCACCCACACC  
AATCCTGAGAACTCAGTGCCACCCACAGCCAATCCCGGGGTGCCCCAT  
TGCCCTCTCTAAAGCCTCCACCCCAATCCGGGGGTGTTCAATGCCACCCCA  
CAACCCCCCTCAAAGCACTCCTGGATAACCCACGGACACCCCAACGCCCT  
AAAACAAATCCCAGGGCGCTCAATGGAACCTCCCGCGCAACCTCGGGCTG  
CCCCACGCCCCCTCCAATCAAGCAGACCCAGAGACCCCCCTTTTCTCC  
CAACCCCTCCGGCCCCACACGCCAAAGGCTCTCAAAGACCCCCCCCCAGC  
GATCCCCGGACCGAACAGGGCTTTGGGGTCCCCCCCCACGGCGCTCCCCGT  
GCCGCCCCCCCCCGCCCCGTGACACAGCACTTTGGATCCCCGCGGGCCCT  
CCCCGCGCGCCGCCCGCGCGAACACCCAAACATGGCGCTTTTCGCCCA  
AAAGCGCCGGGCACAAAGCGGCGCCGCCCATTTGGTCTGTGCCCCGGCTC  
CTCGCTTCCCATTTGGCCCCCTTCGACGGCGGAGGGGCGGAACCAGATTGA  
TGGACAGCTCATGCTCACGTGTCTCCCCCCCCCGATTGGGTCTTTTT  
GGTTAAAAAATAAAATAAAATCATAAAAAAGGGCGAAGTTGCCCCATC  
GTCACTCACCTGAGCCGCTCCACGCAGGGCCACGACCCCAACCCGATA  
TCATCCTCGCGCTCGCCCCCTTAAAGCCCCGTTTTTGGGGCAAAAATCAA  
AAAAACATCCCAGGGCAGAAAAAGGAGCCACGCGCTACGTGAGCTGCAC  
CGTGATTGGCCACCCGCCGTACGTGACGGCCCCGCGCCACTCCGACGGC  
CCCATTATGAGGCCCGGGCGGCTCCGCGGGGTCTATCGCCGCTCCGGA  
GGGGGTGATGGCGCGCATGCGCAGTGACGGGGGCATGTGGTGGGGGGAGG  
GAGGGGTGGGGCTGTGGGGATGCCCGGTGTTGCTGGGGGGCTGCTGTAGG  
GTTGCTATGGCATTGCGAGGATGCAGCCATGAAGATTCACGGCATTGTAAG  
TGTGCATCTGTAGGGGCCCTGGCATTGCAAGTGTGCACCTATGGGAGTG  
CCCGGCATTGCAAGGGTGCACCTCTGGACGCGTTTGTATTGCAAAGGGT  
GCAGCTGTGGTGGTGAATGGCATTGCAAGGGTGTATCTATGGGAGTGTAC  
AGCATTGCAAGGGCGCACCTATGGGTGTGCTTGGCATTGCATGCATGCAC  
GTGTGGGGATGTATGGCACTGGGGGGGTGCACCAAGTGGGGGTGCTTGGGA  
TTGCAAGGGTGAAGCCTATAGCAGTGCCTGGCATTGCAGGGTTGCACGCAG  
GGATGCGTACGGCATTGCAGGGGTGCAGCTGCCGGCATTGCAGAGGGCCG  
AACCCGCCCGTACGGTTGTGACGCGCTTCCAGCTCGGAGGGCGCATTGCA  
GTGCGGTGAGTGCAGTGCGAGGAGCCACTGCTGCAGGGTGTACAGTGCA  
CGCCCCGAGGATGTCCCCCTCGGCTCCAAACCCCAAAACCCACGCTTATT  
ACCCCCCAAAACATACTTTTACACACAAGACACATTTTACCATCAAAC  
CTCACGCTTTTCCCCAAAATCCCTCACAAAAACAAAATCCGCGCCGTGA  
TGAGACACCCAGAGATCTACGGAGCCTACTCGTCCCCTGCTTCATTAAT  
TAGAGCTGCTTATTAATTGCTTGGGGGTGGCTCAGCGCCTATTACAGCGT  
CGGGGCTCCCCGCTAGTTTCTTCTATCTAGTAACAAGTGACGCAAGGTAA  
CTGCGGAGCGCGGCCATTGGTTGAGCCGCACGATCATCTCCTGTACAGC  
GCTGGTGTCCCCGCAGATCTGTTCTGCCTAGCAACCGATGACGCGTAAA  
GCCGCGAGGCACGGCCATTGGCTAAACTGGTTGCCGGTAGCAGAGGGATG  
GGGGCTGCGAGCGGGCGCGGGCGCTCGTGGCAGCGCTCTCGGGGCGCGC

FIGURE 10

SUITE 49

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E1REV.txt

CCTGGGGAGCGTCAGAGCCGGTAGGGGACGAGGGCGGGGGCGGTATGGG  
TGGGCACGGGGTAGTGCCAGGGGTGTCCAAGATGTGTGCATGGGGAGTGC  
AAGGGGCTGTGCAAGGAGTGAATGATGCACTGGGGCAAGGGGTGGGCATG  
CACTGGGGCAAGAAGTTGTGCAAGGGGTGTTTGTGCATTGATGCAAGGGG  
AGGATGAGCAGGACTGTGTTTGCATGCATGCAGGGGGTTGTGCATGGTGT  
GATTAGTGCATTAGTGCAGCGGGTTGAGTGTGAGATGTGGAGTGTGTGC  
AGTTGTGAAAGGGTTGCCATGCACGAGCTGATGTGCGCTCAGTGAGCGTG  
CACGCAGCCTGCAGAGTGGGTACACCTGCAACGAGCATGCATGCAGCAGA  
TGTGTCCATGCACAGTGTGTGTGTGCTGGTGTGTCCCATGTCCAC  
GCCCTGTCTGTGCTGCAGAGCCATCGCTGCACACTCTGTCTGAGGTGCT  
CTTCTGCCAGCCGGACACGCCGTGCTGGGGCTGTGAGTGGCCTTCGACT  
CAGAGCAGCTCTTCTCATTGATGTCCCAACTCGCAGTGGCTGCCGCAG  
CTCCCCGATGGCCCCCTCGTGGCCCCGAGACATCGAGCAGCCCCACGAGCT  
GCTGCACGACGCCGCGCTGTGCCGTGAGCTGCTCGATTGCTCACCAGAA  
TCGCCACCGGGCCAAACCAATGCCCTGAAGCCAAGGGTGGGTGCTGCTGT  
CCCCGCTATGACCCCACTGATGGGTCCCCAGCCGTGTGTTCCCAGTGATG  
CTGACCCCAATGGACATCCCCAGTTGATGCATCCCCATTGATGCATCCCC  
CACAGACATCCCCATTGATGCTGTCCCCATTGATGTGTTCTCAGTGGATA  
TCCCCAATTGATCCTGTTCCCAATGATGCTGTCCCCAATGGACATCCCCA  
TTGATGCTGTCTTGTGTAAGTTGTCTCGATTGATGCATTCCCATTGATG  
TGTTCCCAATGGACATCCCCAGCTGATGCTGTTCCCACTGATCCTGTCCC  
CATTGATGCATCCCCAATTGGTTTATTCCCCATTGATTTATTCCCCATGG  
ATGTCCCCACTGATGCTATCCCCAGTAATGCTGTCCCCACTGATGCTGTC  
CCCAATGATCCTGTCCCCAGTGATGTGTGTTCTAATGGACATCCCCAAT  
GATGCTATCCCCAACGATGTGTCTCACTGATGTGTCCCCAGTCCATGTG  
GTTCCCAGTGATGTGTCCCCAACAAATATGACCTCACTGATGTCTCCCCAG  
TTGATGCAATCCCCAATGATGCATCCCCAACAAATGCATTCCCCAATGATAT  
TTCTCAATATGATGCTGTCCCCAATGATGCATTCCCCATTAAACGCACTC  
CCACCGACGCATTCCCACCGATGTGTCCCCACTGATGCGTCCCCACTGAT  
GTGTCCCCACTGATGTCCCCCCCCACAGGCATCCCGGTGGCCGACGTCTT  
CCTGCAGCAGCCTCTCGAGCTCGGCTACCCCAACACTCTGATCTGTATGG  
TGGGCAACATCTTCCCCAGCCATCACTATCAGCTGGCAGCGGGATGGC  
ATCCCCGTACCGATGGCGTCACCCACCTCACCTACACCCCCACCGAGGA  
CCTGGGCTTCATGCGCTTCTCCTACCTGGCGGTGACACCGCACTCTGGTG  
ACATCTATGCTGCAATTGTACCCCGGAGAGGGACAACATCTCTGTGGTG  
GCTTACTGGGGTGAGTGGGGATGTGGGGGTGCTGCTTTGTGTCCCCGCAG  
CGGTGGCTGATGGGGGCGGGTGGTGGGAGCAATGCTTTGTGTCCCTGCAG  
TGCCACAGGACCCCATCCCTTCGGACGTGTTGGCCACGGCGGTGTGCGGC  
GCAGTGACGGCGCTGGGCATCCTGCTGGCACTGCTGGGTTTGGGGCTGCT  
GCTGTCCGCCCGCGCGCAGTATGTGGGGACAATGGAGACAGCAGGGAC  
ACCCGCCCGTACTCACTGATGTCCCCCATAAGTTGATCCCTCGGTGTGG  
GAACGGTGATGGTGATGTAATTAAGCCCTTCATTTGCAGCGCGGTGTCC  
TTGTTTGTCCCCACTCCGGGAAGGGTGGCAATTAATGGGGTTGGGCATTG  
TCCCCATGGCCCCAGGTGGCAAAGTCTGATCCCATTCACCGCCCATGGG  
GTGACGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG  
AGGTGGCACGGAGGGGATGAAGGCAGCAGTGCTCCTGATGGGGCCAAGGG  
GTTTCAGGGTGCTGGGGGCGATGGGGCTGGTGTGAGCTGCGGGACAGCA  
GGTAGGATGTGGGGAAGTGTGGGGTTTTTGGGGTGAAGCATGGGGGTTTT  
AGGGTGCAACATGGGGTTTTTGGGGGTGCAACATGTGGGTTTTGGGGGTGCA  
GCATGGGGGTTTTAGGGATGCAGTGTGAGTTTTTGGGTGCAAAATGGAG  
TTTTTGGGGTGCAACGTGGGTTTTGGGGGTGAGTATAAGTTTTTGGGTG  
CAACATGGGGTTTTATGGTACAGCGGGGCTTTGGAGTGCAGCATGGGGT  
GCTGCATGTATGCATAGTGCACAACATGGGGTCTTGGTGTGAGTGTGA  
GTTTTTAGGGTACAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT  
GTGCAAGTGAATTATTAGGGTACAACATGGGGTTTTAGGGTGGCGCACA

FIGURE 10

SUITE 50

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E1REV.txt

GGGCTTTGGGGCACAGCCCCAGTGCTGTGCCCTCCCCATGCCCCAACGC  
AGGCGCCTTCGTGGTGCACATGGCCAGCTCCTGCCCAGTCTGGCCAATG  
GCTCCCTGGGCAGCTTCGACCTCACCATGGCCTTCAACAAGAACCTCTG  
CTGTGCTACGACCCCGACGTCCACCGCTTCTACCCTTGCGATTGGGGGCT  
GCTGCACACCGTTGCCACTTTGCTCGCCGCCATCCTAAATGATGATACCA  
CATGGGTGCAGCGTGCAGAGGCACGCAGGCAGGCGTGCACTGAGCTGGCT  
GCACAGTTCTGGACACACACAGCACTGCGCAGGAGTGAGCACCGCTGCAT  
GCAAGTGGAGCATTGCAAACACGGGACGTTGCATGGGGGTGTTGCATGGG  
GGTGTTCGAATGGGGTGATGCACAGCCGGTCATTGCATGAGACGCTGCAC  
GGGGATGTTGCAAAGGGAAGTGCATGGGGACATCGCACAGCAGGTTGAAT  
GGGATGTTGCATGGGGACTTTGCAAGGGAAGTTCGCACAGAGCATTGCAG  
GGGATCCACGCAAGGAATTTGCATAGGGAATGCACAGAGATGTTGCCTGG  
GAATGCTGCATGGGGTCATTGCATGAGGAAGTGCAGAGAGACATTGCACAA  
GGAAATGCAAAGGGGCATCACTAGGGGACATGGCATGGGGCATTCTAGGG  
AGCATTGCATGGGGACATTGCAAAGGGAATGCAAAGGGACATTGCATGGG  
GACATTGCAAACAAATTGAGTGGGAGATTGCACCGGGATGTTGCATGGGG  
ACATTGCATGGAATGTCCACCAACCACCCTGCAGGGTGACACTGGGACC  
ATCCCCAGCTCTGACCATCCCCCTTTGCTGCAGCACCACCCAGGTCCG  
CATCGTCCCCATCCCCATCTCCAACGACCCCGACACCGTCCACCTCATCT  
GCCATGTTTGGGGCTTCTACCCACCCGCACTGACCATCCAGTGGCTGCAC  
AACGGCCTCGTGGTGGCCTCAGGTGACACCAAAGTCTGCCAACGGGGA  
CTGGACCTACAGGACACAGGTGGCCCTGAGGGCCAGCACTGCAGCAGGGA  
GCACCTACACATGCTCAGTGTGGCACTCCAGCCTGGAGCAGCCGCTGCAG  
GAGGACTGGAGTGAGTTTGGGGATGGGGATGTGGCACCCACACCCACAG  
TCCCCACGGCTCATTGTGCCACGCTGTCCCCACAGGTCCCAATTTGTC  
CCCGCGATGATGGTGAAGGTGGCAGTGGCGGCCATGGCGCTGACGTTGG  
GGTTGGTGGCACTCAGCGCCGGGGTTTTTCAGCTTCTGTGAGCGGCCACGG  
GGTGAGGGATGGGGATGTGGTGTGGGGACATGTGTGACACCGAGGGTCT  
GGTGTCCAGTGTGGGGGTGTACCTCCTCATTCATCATCTTCTGTGTGGCAG  
CTCCTGGCTGATGCTCCAGTCCCGTCCGTGATGCGGGTTCTCACTCCAAT  
CCTGGTCCCCAAAATGATCCCGGTCCAAGTTCTGGTCCCCATCCAGTCC  
TGGTCCCCATTCTGGTCTTGGTCTGGTCTGGTCTGCTCCTGGTCCCT  
ATCCCTGACTCTGGTCCCGGTCCCCATCCCGATGCCAGTCCAGTCCCTGG  
TCCCCATCCTGGTCTGCTCCTTGGTTTGGGGACCTCAATGACTGGAAT  
CCCATGTCCCAACATGGGGACCCACAGTTTGGGGTGAGGGGCTCTCAGCC  
CCCAATAAAACCATCTGCAGCCCCAACCTCGCTCCAATTCTTCGTTCCCA  
CGTTGGGTGGGTGGGGCTCCAGTGTCTCCAGTGTCTCCAGCCGTCTATG  
TCCCGTAAGCGTCGGCTCCACTGCATTCTGCTCCGAAACAGATGACGCT  
ACCACGGCGCCCGCTCTGATTGGCTGCTCCGTGCCCTCTCTCCGTCCAC  
GTCCGTGAAGGGGGGGATGTGGGGTGAGGGAGCTGAGGGGGCCGCCCT  
TCCCCCCCCCGCTCCCCCTCCCGATGTTGGTGTATTGGGGCTGCTGC  
TGGGAGCGCGGGGGCAGGTGGGGGTTTGGGGTGGGGTGTGGGGGGT  
CTCTGCCTAATGAACTCTGGGGGGGGGGACGTGGGGGTCTCTGCTTTA  
TGGGACTGTGTGGGCGGGCTTGAAGGGGCTCTGCTTTACGGCGCTGGGTG  
TGGGTTCTGGGAAGACTGTGCTCTATGGGATCATGGTAGGGGCTTGGGGG  
GGCTCTGCTTAATGGCACTGTGTGGAGGGACATTGGGGGTCTCAGCCTTA  
TAGGACGTTGGGGATGATTGTGGGGGTCTCAGCCTTTGCAATATTGAGG  
ACACTCTGGGTGGTGGTCTGAGCCCTTAGGGCCCCCAGGGAGGGCTTAG  
GGTGGGCTCAGCCTTTTGGGATACTGGGGTCTTTTGGGGGAGGGTCTC  
AACTTTATGGGATGTTGCAAAGAGTTTGGAGGGGTCTCAGCTCTGAGGG  
ATATTGGGGACAATTGGGGGATCTCAGCCCTTTGGAACCTCAATGGAGGA  
TTTTGGAGTGATGCTGAGGACTCAGCCTTTTGGGTTGCTGGGTATGATT  
GGGGATGCTCAGCCTTATGGAATGGTGGGGACACTTTGTGGGGAGCTCAG  
CTCTGTGGGATATTGGGGCACTTTGGGGGAGTCTCAACCTTTAGGACTC  
CCAGGGAGGGG

FEUILLE DE REMPLACEMENT (REGIE 26) CAGCTC

FIGURE 10

SUITE 51

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E1REV.txt

GATGTTATGTCCCCATGGGGACCTCTGGGGGCTCCAAATGGGGATGAGGT  
CGCTGCCAGCACTGCCATCTCCCTCTGTCCCCCAATGCAGGTGCCTTC  
ATGGTGCATGTGGCCAACTCCTGCTCACTGGCAGCCAATGGCTCTCTGCG  
GGGCTTCGACCTCACCGTGGCCTTCAACAAGAACCCTCTGGTGTGCTACG  
ACCCCGATGGCCACCTCTTCAACGCCTGCGACTGGGGGCTGCTGCACGGC  
GTGGCTGGACAGATTGCCATTGCCCTCAACAATGACAGCACCTGGGTGCA  
GCGTGCAGAGGCACGGAGACGGGCGTGCAGCAAACTGGCTGCACAGTTCT  
GGGCACAGACGGGCGCTGCGCAGGAGTGAGCATTGCAATGGGGCTGTTGC  
ACGGGGCGTTGCGTGGGGATGATGTTGCATGGGGCATTGCATGGAGATGA  
TGTTGCATGGGGTGTTGCATGGGGACATTGCATGGGGCATTGCATGAAGA  
TGGTGTGTCATAGGGCGTGCATGGGGATGTTGCATGAAGATGTGTAGCA  
ATGATGCATGGGGCATTCCATGGGGACGCTGCATGAGGGTGTGTTTAGC  
AATGATGCATGGGGTGTGTCATGGGGATGTTGCATGGAGATATTGCATGG  
GGCATTGCATGGGGTTGATCCATGCAGCGTTACATGGGGTTCTCAAGCAG  
GGGGATGTTGCATGGAAAAGTTGCATGGAAAATTGCACAGAGGTGTTGCA  
AAGCATATGCATGGGGATGTTGTATGGAGGATTGGACGGTGGCTTTGAAG  
AACATTCTGCATGGGGCATTGCTTAAGGGTCCCAAGCATGGGGATGCTGC  
AAGGAAATGCTGCTGCTTGGTGGCCTTGCAGAGTGTGTTGCATGGAGTTT  
GCTTCAAGGAGATGTTGCATGGCATATCATCTGCAGTTTTCAGAGCACA  
TTGCATTGCACATTGCACACTGCACAGAGCAGTGCACCTGGGCATCTCCCA  
GCGTGTGGCACAACGCTGTTGCAAAGGACATCCCACGAGGTGTTGCAGCA  
AACAATGCGCAGAGCTTGCACAGAACGTGGGATATCCCATGGGGATGTGG  
CACAGAGCATTGCGTGGGGAATCCTACAGGGAAGTGAGATGGGGAAGTTG  
CACAGAGCGTTGCAAGGGGTATTGCACAGAGGGAACCTGCAGAGAATGGG  
GCAGGAACCGTCCCCATCCCTGCTGCTCACCATCCCTGTCCCCACTCCA  
GCTCAGCCCCAGGTCCGCATCGTCCCCGCACAGACAGGGAACCCAGCGT  
GCCCCCTCCCTCACCTGCCACGTGTGGGGCTTCTACCCCCCGAGGTGA  
CCATCATCTGGCTGCACAATGGGGACATCGTGGGACCTGGAGACCACTCA  
CCCATGTTTGCCATCCCCAATGGGAACCTGGACCTACCAGACACAGGTGGC  
CCTCTCGGTGGCCCCAGAGGTGGGGGACACCTACACGTGCTCGGTGCAGC  
ATGCTAGCTTGGAGGAGCCCCCTCCTGGAGGACTGGCGTGAGTTGGGATCA  
AGGGGGTGACACAGGGACAGCGGTGTCCCTGCTGTGTCACTGCTGGCTGT  
GTCCCTGCAGGTCTGGGCTGACGCTGGAGGTGACGCTGATGGTGGCTGT  
GGCCACTGTAGTGATGGTGTGGGGCTCAGCTTGCTCTTCATTGGTGTCT  
ACTGCTGGCGGGCCCAACCCCTGCCCCAGGTGGGTGCTTGAGAGGGACC  
CTATGGGGCTCCATGGACCTCTAAGGGGTCTCTGTCTGGTTCTATGGGT  
CTCTGGGTGCTGTGAATCTTTCTTTCTCTGTGGGTCCGTCTGGGGTAT  
CTGTTGATCCCTATGGGTGCTGTGGGGCCTCTGTGGGTCTCTATGGGTC  
CTTCTGTTGGCCTCTGTGAGGTCTCTATTTGTCTCTATGCATCCCTTTGG  
ATCTCTATGGGGTCTCTGCGGGTCATTACGTGTCTCTATGGGATGTGACC  
ATTTTTGACAAGAACCCCACTCACCCCTCTATTCCCCAACAGGTACG  
CCCCGCTTCCCGGTCACTACCTTACAGGTAAACAGTGTCCCCAACTG  
TCCCTGTCCCCATTGCCATCAATGAGGGCTGAGTGACCCCATCTCTCACC  
CCATGTCCCTGCAGGCAGCATCTGATGGACACCTTCTGTACCAACTGTC  
CCTGCGTGTCCCCATCCCTGACTCTGCGCCGTGGTGTGACATTAAAGAC  
ACTCTGCAGCCTCTGTTGGTGTCTCTGTGGGCTTTTGGGGTGGGGTGGTG  
TCACCGGGGAGAGGTGAGGTGGGGTCAATTGCATCCATGATGGTGATGGT  
GATTGACATTGTGCACAGGGAGATGTCCAGGCGCCTGTGGGGTCTGTGTT  
TAGGGCCAGTTCTGCTCAGTGCCTCCGTAAGTGATCTGGATAGGTCTGTC  
AGTCATCCTAATTAAGGAGGGGACAACAGTGAATGGGGAGGAGCCGATGA  
CTCAGGCTGGGAGTGGTGATCCCAGAGGTTTCTCTGCTGTGAGTGACTC  
CGTGCTTTTCGCTTTTCGCTTCAACAACCTGAGGGAGCGCATTCTGCTGGCG  
CCCGATGACGTACATAAAACCCCGACTGCCATTGGCGGAGAGGCGACGG  
AGGAGCCAATGGGGGCGCGGGGCGGGGCGGAGGAGGAGGAGGAGGAGGAG  
GAGCTGCGCTGGGTGCGGGGACTTGAGAGTGCAGCGGTGTGAGGCGATG

FIGURE 10

SUITE 52

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ElREV.txt

GGGCCGTGCGGGGCGCTGGGCCTGGGGCTGCTGCTCGCCGCCGTGTGCGG  
GGCGGGCGGCGGTGAGTGCGGGCCGGACCGGGACCCCTCCCCGCCGTAAC  
CCCACCCCGGGGCTGTGCCCCTGGGATCCTCAGACCCCCACCCGCGGCTC  
ACGGCCTCGCTGCGCTCCGCCCCCGCAGAGCTCCATTCCCTGCGGTACGT  
CCATACGGCGATGACGGATCCCGGCCCCGGGCTGCCGTGGTTCTGTGGACG  
TGGGGTACGTGGACGGGGAACCTTTCGTGCACTACAACAGCACCGCGCGG  
AGGTACGTGCCCCGACCGAGTGGATGGCGGCCAACACGGACACAGCAGTA  
CTGGGATGGACAGACGAGATCGGACAGGGCAATGAGCGGAGTGTGGAAG  
TGAGCTTGAACACACTGCAGGAACGATACAACCAGACCGGCGGTGAGCAC  
GGCCGGGGCGCGGCTCCGTGGGTGTGGGATGGGCTCCATGGCGCAGTGC  
CGCCACACCCCCAGGCCTGGCCCTGCCCGGGCGGACCGTCCCGGGGCT  
GCCCCTCACAGCCCCACCGCGCTCGGGGTGCCGCGTCCCGGGGGGACCCC  
AACCCATCCCCGCTGCACTGGGAGCCCCGGAGCCGGAGGGGGCCCTCACC  
CCCTGCCCGGCTGTGTTTCAGGGTCTCACACGGTGCAGCTGATGTACGGC  
TGTGACATCCTCGAGGATGGCACCATCCGGGGGTATCATCAGACAGCCTA  
CGATGGGAGAGACTTCATTGCCTTCGACAAAGGCACGATGACGTTCAGT  
CGGCAGTTCAGAGGCAGTTCACCAAGAGGAAATGGGAGGAAGGAGGT  
GTTGCTGAGAGGTGGAAGAGTTACCTGGAGGAAACCTGCGTGGAGGGGCT  
GCGGAGATATGTGGAATACGGGAAGGCTGAGCTGGGCAGGAGAGGTGAGC  
GGGGTGGGGTGGGGGGGGGGGGGGGGGGCGGACGAGTGTGGGGCTGGACGT  
GGGGCGGGGGCTCATCGTGGGGAGCTCAGCCCGGCCCTCACTGCCGCCCA  
CCCACAGAGCGGCCTGAGGTGCGAGTGTGGGGGAAGGAGGCTGACGGGAT  
CCTGACCTTGTCTGCGCGCTCACGGCTTCTACCCGCGGCCCATCGCCG  
TCAGCTGGGTGAAGACGGCGCGGTGCGGGGCCAGGACGCCAGTGGGGG  
GGCATCGTGCCCAACGGCGACGGCACCTACCACACCTGGGTCAACATCGA  
TGCGCAGCCGGGGGACGGGGACAAGTACCAGTGCCGCGTGGAGCACGCCA  
GCCTGCCCCAGCCCGCCTCTACTCGTGGGGTGAAGTGGGGGATGTGGGG  
CTGGGGGGCTGCGGGCTGCCCCCTTCCCTGCTGATGGCCCCGCTCTCCCC  
CAGAGCCGCCACAGCCCAACCTGGTGGCCATCGTGGCGGGGGTGGCCGTC  
GCCATTGTGGCCATCGCCATCGTGGTTGGTGTGGATTTCATCATCTACAG  
ACGCCACGCAGGTAAAGCAGAGGGGTGCAGGCGGGCAGTGGGGGCTGTA  
GGGGGATCTGGGTCCCCCTTGGGAGCCCCCAACCTGGCTGTGATGTAAC  
CTGTGATGAAGCATCTCTGTCTGTCAGGGAAGAAGGGGAAGGGCTACAA  
CATCGCGCCCGGTGAGTGTGAGGGCAGCGCTGTCCCCACCTCTGCCCA  
GTGCCAGGGTGGTCTGGGTCCCTGCTTTCTCCAAGGTACCCATTCTCT  
GGTGTGGGGCTGCTCCATGCCCCATAGGGAGCACAGGGCTGGATCTCA  
CAGCTGTTCTCCCTTATAGACAGGGAAGGTGGATCCAGCAGCTCGAGCA  
CAGGTGCGGTGTGGGGCTGTGGGTGGGAGGGGTCCGTGTGCTCTCTGTG  
GTACTGCCCAGGGCTGGGCTATGCTGGGGCTCTGCGGGGAGACCCCGGA  
GCAGAGGGTTGGGATGTGAACCTGGCCCCGTGGGACATCATCCCTCTCA  
TCCCCACAGGGAGCAACCCCGCCATCTGAGTGTGCTGTGCTTCAGCTGCAA  
GGAGCCAACAGTCCACACCAGCATTTGGGGTGGTGTGACACAGCCCC  
ATCCTCCTGACCTCTCACATCTCATTCTGCTTCTATGCTGACTGTTATG  
CTTTGCTGCACTGCTTCTGTGAAATAAATGATGGGCCATTCTGTGCT  
CAGCTTGCTGCACTGTGCTGTGGTTGGGGATGGGGTGGGTGA  
GAGGACCGTGTCCAGTTTGGCTGCTCAGGGTGCAGATGTGGCCCTGTGC  
TGAGTACCCACAGCCCTCCCCCCTATCTGCCTGCTGCTCACTCCCCCTT  
CTGTACCCCATCCCTTCTCACCTCTCCTCTGTGACCCCATGCTGGTGGT  
TGCTTGCTCCCTGTCTGGCAGAACTCTCATTTTCCCAATGGCATCCCTG  
GGTGTGGGATGTGGTCTCCTTGGTCTCCCCCAGCAGTCACTGCACAT  
ATCCACCCCACTTCCCCCAGGTTGTTGTCCACAGCACTCCTATTTCC  
CTCTCCCCCCCCCCCCCCCCCCCCCGCCATCCAGCTGCCTCTGCAATC  
CTCACCTTGCCACACACAACCTTTGCGCACTCCACCTCCCTCATCCCGC  
CCTTCCCCCAGCTCTCCTGTCCCTGCTGGCCCCCTCCCCCCCCCATT  
GTACCCTA

FIGURE 10  
SUITE 53

E1.REV.txt

FIGURE 10

SUITE 54



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GTCAATGTCCCCCTGTCCCAGTGTCCCACAGCTGTGCTATCTCTGTGCT  
ATGTCCCCTCATGCCATCATGTTCCCAGTGTCTGGAGCCCCCATGCCGC  
CCCATTCCCACGTCACTGCATCCTCCTGCCCCAGAGCCCCCTGAACTGTTG  
TGCTGTACATCCTGATGTCCCCATGCCATCAAATCTATGTCCCACAGT  
CCCCATGCCATCATATCCCATGACCTGCCATCTCCACACCATTATGGCC  
TCCAGCCCCGTTGGCATTCTGTCCCCATCTCCTGACATCTCAATTACATCA  
CGTCTCCACATCTCCCAGCCCTATCCCACCATGTCCCCATGCCCCCAGT  
CCTATCCTATCATGTCCCCACATCCCCAGCCCCATCCCATCACGTCCCC  
ATGCTATTGAGCCACCCCATCCCATAACCACTGGTCCAGAGAGAGGCAG  
TGTAAGAGGGCCACATCCTTCTTCTCCAGGCGGTGGCTCTGCTGCAGGCGC  
TGCCGGTAGTGTGCAGCCGCCCCATCCTCATTGGCAAAGCTTCGCACAGT  
GGCCATGGCCTGGAAGGTCTCCACTGCCACCTCGCTGGCCCGGGCCTGCG  
CCTTCTGCATCTGTGGTGCCAGGGCCTGGGGACAGCAGTGTCTTGCAGG  
GCGGGTGGGAAGGGAATGGGGGCTGGGGAGGGGACAGTGCATGTATGGAG  
GGAACAAAGAACACGTGGAGGGGATGGAGGGGACATAAAGGGGACGGTGG  
GCATGTGGAGGTGACAGTGGGGGCATGCAGAGAACAGAACCCATGTGGAA  
GGGATAATGGTCACACATAGGGAATAATGAGCACATGGCACGGATGGTGG  
ACGCATGGAAGGGGCATGGGGCACGTGGAGGGACAGCGGTACACAGAGG  
GGACAACAGCAGGAGGATGGTGGGTACATGGAGGGGACAGTGGGCACATG  
GATAGGGCAATGAGTACATGGTGGTGACACTGGGCACATGGAGGGGACCA  
GAGGCACATGGAGGGGACCAAAGGCACATGGAGGTGCAGACAGCAGCCCA  
TACCTGCCGGAAGTGCCCCACAGCCCTGGGCAGTGCCAGCAGCAGTGGCA  
GCGCCAGCGCGGTGAGCAGCGCCATGCGCGGGGACAGCCAGGCCATGGTG  
GCGAAGAGGCGAGAGGCCACGTGCCAGATACCACAGCAGGAGGCTCAGCGC  
CTCACCCAGCGCCTCGCGCACGTCTCCGCATCCCGCGTCACCCGCATGG  
CCACATCCCCTGCCGGGTGACAGCGCCGTGAGTGCCACCCCTGTCCCTTA  
TCCCCGTGTCCCCTCCCAGCCCGGTGCCCTCACCGGCCCCGTGCGCGCG  
CAGCTCGGTGATGCTCTGCCGACGAGCGGCGGCAAGACGCGGCGCTGGA  
GGCGGCTCTGCGTGCGGCTCAGTGTCCCCACGAAGGTCACATCACACACC  
AGCTCAGTGACAGCGCTGTGACGGCAGTGGGGTGTGAGGGGGTCCCAGCG  
TGCCCCCTGCCGCGACCGCGTCCCCCTATGCCAGTACCTGCTGAGGCCC  
AGCAGCACCATGGGACAGGATGGCTGCCAGTCTCCTCGCGGGCCACCCA  
GTCGCTGGCTCGCCCCATGTAGTAGGGCACGGCCATCTCGCCTGTACCA  
CAGCAGGGTCAAGGCATGGGGGACCCCCGAGGAATGGTGCCCCAGGAG  
TTCTGTGCTGCACCCCCAGTTTGGTGTGACCCCCAAAGCTCAGAGGTG  
AACCTCCGAAGCTCATTGTTGCCCTCCAGTTGGCTGCAGCCCCCAACCC  
ACCGCAAACCCATCTTATTCCCATTCAATCACCGCCCCCAACCCAAACCC  
GACCCCAATTCTATCTCCATCCCCATCCCTACCCCAACCCCAACCCCATTT  
CTATTCTATCCCATTCTATCCCAACCCCAATCCAACCCAGTCCCATCT  
CCATCCACACTCCATCACATTCCCATTCCCACCTGTCTTCAATCCCCAT  
TCCATCTCCATCCCAACTCAGCCCCAGTTCCCATTCTCTCCCCATCCC  
CACCCCATCTACCCAGTCCCAATCCCAGTCCAAACCCACATCATTACC  
ATTCCATCCCAACCCATTCCCAGTGCCAGCCTATACCCATCCTTACCC  
CCACCCCAATCCCATCCCATTCCCATCCCATTCCACGGCTACTTCCAT  
CCCCAATCCCATTCCATCCGGTTCCCAATCCCATCCCCATCCCTACCCCTT  
ATCCCCAGCCCCACCACAACCCCATCCTCATTCAAATCCCAACCCCACTC  
CGATCCCCTCCCCTCCCCCGCCCCGTACCCAGCGCCGAAGCCGCCAT  
CAGACCCATCACCAGCGCGCAGCGCGCGCTCCGGGCTCAGCGAGAGGA  
GGAGGCGCGCAGCCGCGCCATCTTCCCCATCGCGGCCCCGATCCCCCTC  
CGGCCCCGATCCCAATGCCCGGCAGCGGCGGAGCTTCTCGGAAACGAGAG  
CGTCTCTCATTGGCTGAGGCGGTGCAGCAGCGACGCTGCTCATTGGTGA  
GATGGTTTTCGCGTCATCAGTTGCCAGGCAGATCGGAACACTGCAGTTTGG  
AGAGGGGCGGGTGATTGAAAGTGAAAGTAACGGCGGAGCGGGAAGGAGAT  
GGAGAGCGGCGCGGTGAGGGGCTGGAGGGGGCTGGAGGGGGATGGACTG  
GTAGGGGCTGGTGGGCTCTG

FIGURE 10

SUITE 55

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ElREV.txt

GTGGGGACTGTGAGGGGCTGGAGGGATCTGATGGGGACTGGAGGGGTTT  
GGTGATCGCTGTTGTGTGCTCCAGGCTGGGCTGTGGGGAGCCGGACTGGA  
AGTGGGGGCCGTTCTAAAAGCACTGCTGTGTGTTCCAGGTGCTGAGGGGA  
GCTGAGGACCTGCACCAGGAGCACCCGGGGAGCCCACCTGGTCCAGCTG  
TGCACCAGAAGCTCTGGGGATCCCCACCCACAGCCATGGCGATGCCGCC  
CTACATTCTGCGCCTGTCTATGCACGCTGCTCCTGGCCGACCTGGCCCTCA  
TGTGGGCCCTGGCCCACTTCTTCCCAGCACTGGCCCATTTGGGCTGGGTG  
GGCTCCTGGCTGGAGGCCGGGCTGCGCCTCCTGGTGCTGGGGGGGGCCGG  
GCAGCTGCTGGCCCCAGGGGACCCGCTGGGGCTGCAGTGCTGCTGAGCC  
TGGGCTCCGATCTTCTGACCTACGGGGCTATGTAGGTCTGCCTGGA  
GCTGCCCCGGTGCTGCTGGCCATGGCAACGCCGCTCCTGGCTGGTGCTGAC  
CCACGGGACAGCTGTGGTGGCATTGCTCACCTGGAGCCTCCTGGTCCCCA  
CTGTGGCCACTGGGGCAAAGGAGGCAGAGGCCTGGGTGGCCCTGAGGCGG  
CTGCTGGCCCTCGCCTGGCCGAGTGGCCCTTCTTGGCTGTGCCTTCTT  
CTTCTCGCATTGGCTGCACTGGGTGAGACCTCAGTGCCCTACTGCACCG  
GGAGGGCTCTGGATGTCTCCGCCAGGGGGACGGCCTCGCCGCCCTTACC  
GCTGCTGTGGCCTCATGTGCTGGCCTCTGCCAGCAGGTAGGGACCCCA  
CATCCCTCCACAAAACCCCATCCACCTCTGGTGGTCTGCTGGTGGGTTG  
GGGTCTCTGTCCATATCTGGGGGTCTCTGATGGGTTCTGGGCACTCCA  
CTGACCCTTTGTGATTGTCTGAAGGTTCTGGGCTCTCCATTGACCCCTG  
ATGGGTTTTGGAGTCGCCCCCAATTCCTTCCAGCTCGCTGTTTGGCG  
GCTGCCGCGGTGGCCTCTTACCTTCATCAGGTTCCGCTTCATCTTGGC  
ACCCGCGACAGCTCTTCTCCAGCCTGGTGTACCGGGACCTCGCCTTCTT  
CCAGAAGACCACAGCAGGTACAGACTGGGGGCACTTTTGTCCCTGTCCCC  
ACACCATAACCCCACTCACCTACTCAACTCCACAGCTGAGTTGGCCTC  
CCGGCTGACCACCGATGTGACGCTGGCAAGCAACGTGTTGGCACTCAATA  
TCAACGTCTATGCTGAGGAACCTGGGGCAGGTGCTGGGGCTCTGCGCCTT  
ATGCTGGGGCTGTCCCGCGCCTGACAATGCTGGCACTGCTTGAAGTGCC  
GCTCGCCGTACCCGCACGGAAGTCTATGACACCCGGCACCAGGTGATAG  
CAGGGATGGGATGGTAGGGTTGGGGTGACAGGGATGGAGGCAATGGCAAT  
GGGATGGGAACAGTGGGAGTGGGGATAGTGAGGTGGGGATTGTGGGGTCA  
GGGTGGCAGGGATGAGGGCAGCTGCAATGGGATGGGAACAGTGGGAATGG  
GGAGAGCAGGATGGGGATCATGGGTCCAACACAGCAAGGATGAGAGGATG  
GAGAAGAGTGGAGCAGGAATGGAAGTGGGATGGCGAGTACTTGGCCATCC  
CATGGGTGCTGACACCCACTGTCCCCCAGATGCTGCAGCGGGCCGTGC  
TGGATGCAGCAGCCGACACCGGAGCGGCAGTGCAGGAGTCCATCTCTTCC  
ATTGAGATGGTACGGGTCTTCAATGGCGAGGAGGAGGAGGACACCGTA  
CAGCCAGGTGCTGGACAGGACCCTACGGCTGCGGGACCAGCGGGACACAG  
AGAGGGCCATTTTTCTCCTCATCCAGCGGGTGAGGCTGACACGAGGGGAC  
ACCCTGGTGTCTGGGTGGGATCGGGACATCCCCGCTGAGCCCCATCCCCA  
CAGGTGCTGCAGTTGGCCGTGCAGGCACTGGTGCTGTACTGTGGGCACCA  
GCAGCTCCACGAGGGGACCCCTCACTGCCGGCGGCCCTCGTTGCCTTCATCC  
TCTACCACTAAAGCTGGCAGCTGCGTGACAGGTGAGGTGAGGCAGTGC  
TCCTCTGCCACCGGATCCCCATGACTGTGGCCACATCCCCGTGTCCCCAC  
CCTGGGTGCTGTGCTGGGGGTACATCCCCATGTCCCTATCCTGGGTGC  
TGTGCCATGCAGGCACTGGCGTACTCCTATGGTGACCTTCTGAGCAATGC  
AGCGGCCCGCTGCAAGGTCTTTGATTACCTGAAGTGGGAGCGAGCTGTGG  
GTGCTGGTGGCACCTACGTGCCACACAGACTGCGAGGCCACGTACCTTC  
CATCGGGTGTCTTCTCGCCTATCCCACTCGCCCTGAGCGCCTCGTCTGCA  
AGATGTCACTTCGAGCTGCGCCCCGGTGAGGTGACGGCGTTGGCGGGG  
TGAATGGCAGCGGGAAGAGCACCTGCGTGGCACTGCTGGAGAGATTCTAT  
GAACCTGGTCCGGGGAAGTGCTGCTGGACGGGGTGCCGCTGCGGGACTA  
CGAGCACCGCTACCTGCACCGCCAGGTGAGGGGGTGGGGGGAGATGTGGC  
TGCACTGAGCAGTGCTGGGGCTGAGCCTCTGCCCTGGGGCAGGTGGCACT  
GGTGGGGCAGGAACCCGTGCTCTTCTGCTCCATTCGGGATAACATTG

FIGURE 10

SUITE 56

SUITE 57

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E1REV.txt

TTATTTTACAGGAAGCAGTGCAGGCAAAGCATAACAGTCAGCATAGGAAG  
CAGAATGAGATGTGAGAGGTCAAGAGGATGGGGCTGTGCCCATCACTGAC  
CCCAAATGCTGGTGTGGACTGTTGGCTCCTTGCAGGCTGAAGCACAGCAC  
TCAGATGGCGGGGTGCTCCCTGTGGGGATGAGAAGGGATGATGTCCAC  
GGGGCCAGGTTACATCCCAACCCTCTGCTCCGGGGGTCTCCCCGCAGAG  
CCCCAGCATAGCCCAGCCCTGGGGCAGTACCACAGAGAGCACACGGACCCC  
TCCCAACCCACAGCCCCACACCGCACCTGTGCTCGAGCTGCTGGATCCAC  
CTTCCCTGTCTATAAGGGAGGAACAGCTGTGAGATCCAGCCCTGTGCTCC  
CTATGGGGCGTGGAGCAGCCCCAAGCACCAGGAATGGGTACCCTGGGAGA  
AAGTGCAGACCCAGGACCGCCCTGGCACTGGGCAGAGGTGGGGGACAGC  
GCTGCCCTCATCACTCACCGGGCGCGATGTTGTAGCCCTTCCCCTTCTTC  
CCTGCAGACAGAGAGATGCTTCAGCACAGGTTACATCACAGCCAGGCTG  
AGGGCTCCCAAGGGGGACCCAGATCCCCCACTGCCCGCTGCACCCCTC  
TGCTTTTACCTGCATGGCGTCTGTAGATGATGAATCCAACACCAACCATG  
ATGGCAATGGCCACAATGGCGACGGCCACCCCGCCACGATGGGCGACAG  
GTTGGGCTGTGGCGGCTCTGGGGGAGAGCGGGGCCATCAGCAGGGGAAGG  
GGCAGCCCGCAGCCCCCAGCCCCACATCCCCTCACTCACCCACAGTA  
GAGGCCGGGCTGGGGCAGGCTGGCGTGTCTCCACGCGGCACTGGTACTTGT  
CCCCGTCCCCCGGCTGCGCATCGATGGTGACCCAGGTGTGGTAGGTGCCG  
TCGCCGTTGGGCACGATGCCCCCGAGTGGGCGTCTGGCCCCGACCCGC  
GCCGTCTTCAGCCAGCTGACAACGATGGGCCGCGGGTAGAAGCCGTGAG  
CGCGGCAGGACAAGGTCAGGATCCCGTCGGCCTCCTTCCCCCACTCGC  
ACCTCGGGCCGCTCTGCGGGCGGGCGGCACTGAGGGCCGGGCTGAGCTCC  
CCACGCTGAGCCCCCGCCCCACGTCCAGCCCCACACTGCAGCCGCTCCCC  
CCCCACCCCGCTCACCTCTCCTGCCAGCTCAGCCTTCCCGTATTCCAC  
GTATCTCCGCAGCCACTCCACGCAGGTTTCTTCCAGGTAATTCTTCCACC  
TCTCAGGTTCACTCTTCTTCTCCATTTCTTCTTGGTGGGAAGTGCCTCT  
GGAAGTGC CGCAGTGAACGTATCGTGCCCTTGTGCAAGGCAGTGAAGTC  
TCTCCCATCGTAGGCCATCTGATAATACCCCGGATGGGGCCGCCCTCGA  
GGATGTCACAGCCGTACATCCACTGCACCGTGTGAGACCCTGAAACACAG  
CCGGGCAGGGGGTGAGGGGGCCCTCCGGCTCCGGGGCTCCACTGCAGCG  
GGGATGGGTTGGGGTCCCCCGGGACGCGGCACCCGAGCGCGGTGGGGC  
TGTGACGGGCAGCCCCGGGACGGTGCCGCCGGGCAGGGCCAGGCCTGGGG  
GGTGTGGGGCGCACTGCGCCATGGAGCCCATCCCACACCCACGGAGCCGC  
GGCCCCGGCCGTGCTCACCGCCGGTCTGGTTGTAGCGCGCTGCAGTATG  
CCCAGGTTCTCGCGTCAATCTGCTCATTGCCCTGTCCGATCTGCGTCTG  
TCCATCCCAGTACTGCTGGTCCGCCTTGGCCGCTATCCACTCGGTGCGGG  
GCACGTACCTCCGCGCGGTGCTGTTGTAGTGACGAAGAGTTCCCCGTCC  
ACGTATCCCCACAGTCACGAACCACGGCTGCCCGGGGGCGGGATCCGTCA  
CGCCGTTTGGATGTACCGCAGGGTATGGAGCTCTGCGGGGACGGAGCACA  
GCGGGGCGGTGAGCCGCGGTGTGGGTCTGAGGATCCCACGGACACAGCC  
CCGGGGTGGGGTTACGGGCGGGGAGGGGTCCCGGTCCGGCCGCACTCACC  
GGCCGCGCCCCCGCACACGGCGGCGAGCAGCAGCCCCAGGCCAGCGCCC  
CGCACGGCCCCATCGCTCGCACCGCTGCACTCTCAAGTCCGCCGACCCC  
AGCGCAGCTCCTTCAGCTTTTCTACTCCTCCGCCCCGCCCCGCGCCCC  
ATTGGCTCCTCCGTGCGCTCTCCGCCAATGGTAGTTGGAGTTTATGTGA  
CGTATCGGGCGCCAGGCAGAATGCGCTCCCTCAGGTTGTGAAGCGAAAG  
CGAAAGCGCGGAGCGGGGGAGGGGATGGGCGCGGTGTGGGAACCCCGGC  
CCTTCGAGCACGGGGGGGACCCCGGGCTGTGTTGCGACGGGGCGCGTCC  
TTACCCCGGGGGAGGGGGCCGAGGGTCTCTGCCGGGAGGACGGGGGCGT  
GAGAAGAGGAGGAGTCACTCTCCATTCCAGTCAAGGAAGTGTGGGGGG  
GGGGTCACATCCATAGGGTTAGAGGCTCCGTGTCCGGGGGGGAGGGGGT  
GTGACAGTGGTGTCCCCAGGGCTTCTTTGGGATCAGTGCCATTTCCCC  
ACAGCGCCGCCCCACACCGCTTCCCCACATCCACGTGGTCCATCTGAGGT  
CGATGCCCTCAGGGTCTGCAGGTGGACCCCAATGTCCACCCCCCAAGTTA

FIGURE 10

SUIITE 58

ATGATTGACCCCAACCCCGCTGTCCCTGCGCCACTGCTCCCATCTGCCCC  
ACACTGCCGGAGCCATGGGGCCTCACTGGGCCTTCAGCCTCTTCCTCCTC  
CTCTTCCTCACTCCCTTAATGAGGGCCAGCTCCCAGGACCCTGAGTATGG  
GGCTATGGGGTGTGTTGTGGGGTAGCTATGGGACTATGAATGTTCTGCAGT  
GCCTATGAGGGACTATGGGGCACTGGTGGGGCTGGGGGCTGCTATAGGAT  
TGGGGTGTGATGGAGTCTGGGGGGACTAAGGGAGATTTCTGTGTGGTTGG  
GTGGGGTTATGGGGCCAGAGCTGGGGGGATTCTATGGACCTAAGGGGTG  
TCTGGATGCTTATGGGATCTGGGAGGGCTTATGGAGCAGTTATGGGGCTG  
GTGGCTCAAGCAGTGTTCCCTCAGGTTGGTGTGCTGGTGGCCCCCGGCGCG  
TGGCCTTGGGGACCCCATGGGGCTGTTGCTGGCAGCTGTGGGGCCGGTG  
ACCGGGACGGTGACTGCATGGGCTGAGGGGGACCGTGGGGCTGGGCCCTG  
CACCTCCAGTCCCATTGCCCCTCACACCCCAACAACCTTCAACCAGC  
TCCTACAAATTGAGGTATGGGGACACCGGGGGATATGGGGACACTGGGGG  
ATGTCCTCTGGGGTGGGGGGTGGGGACACCCCTGTGGCACACAGGGAT  
GTGTGCACCCCTGGGTCCCCTCCTGCCATGTCACCCATGTACCTCACAT  
CTCCTTCCCCAGAGTCCCCCATGTCCCCATAACCCAAACACCTCCTGC  
TGTGTTCCCATGTCCCTTATAGGTCACCCAGTGCAGGCAGAGCGCTGTG  
GGGCGCTGTGGGGTGGGGGTGCTCCTGGAGGCCACAGCTCCCATCTG  
CCCCCCCCCAGTACCAGGAGTCTGAGTGTGGCCCTGGGGGGCGCGGGG  
TCACCTCATTGTGCAGACAGACAAACCTCTCTACGCCCCCGACAGACTG  
GTGAGTGTCTCCACGTCCACCCTAAAGCCATCCCTCATCTGCCACAGTTC  
TCCCCCAGTGGCCCAAATGCTCCAATTCCCCCTAAATCAACCCCAAAT  
CTCCCCAAAGCCCCCTCAAATCTACCATGAATTCCCCAAATCCACCCATT  
TTCACCTACATTACCCATTTACCCCAAATTCACCCCCAGCACACCCCA  
AATACCCCTGGTCACCCAAAGTCCCCCAAATCCCCTTCAAATTCCTAAA  
TCCATAACCCCATCTGTCCCCATGTGTCCCTTGTCCCCAGTGCCTTC  
CGGGTCTTCTCCATGGACCCCGACCTACAGCCGAACCCCGAACCTGTCT  
GGTCACCATCACGGTATGGGCCCTATAGGGCTGGGGCTGTGGGTGACCCT  
GTGGGGTTTGGGTGACCCTACAAGGCTGTGTACCCCATGTACCCCCAGA  
ACCGTTGGGTGCACGAGTGCAGGGAGGTGCAGCGGGTGGCCCTGGACACG  
GTGCTGAGCGACAGCTGGTGTGCTGACATCGCCCTGTGAGTGGGGCT  
ATAGGGGGCTACAGAGGGCTGTGGGGTGCAGAGGGGGCTATGGGGACTG  
GGGACTATGGGGATTTGGGGCTACAGGGGCTGCAGGCGGGCTAGAGTAGT  
GGGGGGGATTATAGGGTTACTGGGGCATTACAGTGGCCATAGAAGCTATA  
GAGGGCTGTGGAGAACTATAGGATACCTTAGGGGCCATAGGGGTCTACAG  
GGGTATAGGTGAGCATGGGGAAACATAAGGGCCATAGCGACTCCGGAGG  
GCTGTAGCACACCATAGGGGGCATAAGGGCCCTGGAGGGCTCTAGAGGAC  
CACAGAGGTGTATGGGAGGGGCTATAGGGGACTATAGGGTATAT

FIGURE 10

SUITE 59

97/110  
E52FOR.txt

ACATGGGAACACATGAGGACAGGGAGAACTGCAGGGACACAGGGACACT  
TGGGGGATAGGGGGATGGTAGTGATGCATGGGGGGGGGCACATGGGGATG  
TGTTGGGGACACTGGGATGTGTGGGGATATGGGGACACATGGGGGAATAT  
GGGGATGAGTGGGGACATATGGTTATTATAGGGATGTATGGAGACATTGG  
GACACATGCAGAGGAGGGGACAAATGGGGACACACTGGGGGACAGATAGG  
GACATGGGGACACCCAGGGAGGGACACCCCAAGTTCCCCCTTACCGGCGG  
CAGTGATGGTTCCTTCTGTGCCCATCCCCCTTGCAGCAGCGCAGTGACA  
CCGTACTGCGGGGTCCCCACCGCCGCCACCCACCACTGCCCCCGCGGT  
TGGGGGGCTGCGGGCGTGGGGGTGCAGAGGGCGGCTCCATGGGTGAGAGC  
CGGTCTGGGGGTTCGTGGGGTTCAGTTCGCAGCTGGGGGGAGTCCGGGGG  
GGGACCCCGAGTGGGGTCAGAGTCCCCAGGGGTCTGCGAGGGAGAGAGG  
AGTGAGAGGGATGAAGGGTCTGAGGGCATGGGGTTGGGAGGGGTGTGGG  
GCGTAATGGGGTCATTTTGGGGTTAATGGGGACACTGGGGACAGTTTGGG  
AGCTATTGGGGCTAATGGGGTCTCTGGGGGACATGGAGGGGACATTGGGG  
ACATTTGGGGTGTAAT

FIGURE 10  
SUITE 60

987110  
E52REV.txt

TGGCTGATGGGCTGTGTCCTATGAGCGCAAAACACCACAATGGGCAGAAA  
AACCTTCCTCCAGAGGACCAACCCCATCTCTATGGCTTCTTGCACCTGG  
CCTTGCCCAAAATTGGGTTATTTTGGAGAAAAAATGGGCCATTTCTCTG  
CTGGTTGTCCAAGCAGCAAGAGATGCTGGCATGAGTCTCACCAAGCCAAG  
AGGTCGTGTGGGACCAAGAGAACTCTTTTCTCTCCATTAATGATGAGTAA  
CTCCACCTTTGGGCACTCTTAAGGTGAAAATCCTCAAATCTGCAATTTT  
GAAGGCGCAGCTCCACATTTCTCATCCCTTTGTTCTGTCCATGGCAGT  
GCAGGCATTCCAGCCCCATCCCCAGCCCTGTGCTCAGTGTCCCTTCGACT  
GGATTGGATTGAGAGGAAAATGCTACTACTTTTTCAGAGGATGAGAGCAAT  
TGGACGAGCAGCCAGAACAACTGCTCTGCTCTTGGTGCTTCCTTGGCTGT  
GTTTGACAGCGCTGAGGACTTGGTGAGGGGGACACAAAAGAGCCACCAAT  
GTATTTTGTCCGCTTGAGGGCCCCCTTGGCTGCTCTTTCAGTGTTTCCTTT  
CTGATTTTGGGGTGAGGAGGTGGATAATGGTTGTCCTGAGGGTAGGTTGG  
GTCTACTCCTCAAATTTCTTCAAGGGATTTAAGGGAAAAAAGATGTTT  
TTTCTATGAAGTAACCAGCTGGCTTAGAGACTGTGAGCTTTGGTGATGG  
ATTGGGCAGTTTCAAGCACTGAGATTATTGGTTGAAAGGGTTCTGCAGGC  
AGTGGCATGCAGGAAATGTCCCAGAGCCCCATGATCTGTTCCCTCTCCTC  
TTTTCCAGAGCTTCACAATGAGACACAAAGGCAGCTCCCCCACTGGGTT  
GGCCTCTCCCGGAAGGCAAAGAGCATCCATGGGAATGGGTGAACCGCTC  
TCCTTTGTCTCACCTGTGAGTTCCCATCCTTGTCTTGGAGGCTGCAGCTT  
CTCCAGCCCCAAAATGTGGATTTCTGGACCTCGGGAGCATTTCTGGAGGT  
GGCTTATGGGGTGAGGAGATGTGGGGAAGGCACTTCGCACCGCTTTGGGT  
CATAGAAGTTCATTGAGAGGCAGAAGTGGCGCAGGAAAAAGAGATTCCTA  
TTTAATCAATTATTTTGTCTGTTTGAATTCACCACTGTGATTTCTCTTC  
CCCCCCCCCAMAACCTGGGGTCTGCCTGTCCGTCTGTCTGTCCATCCA  
GGTTCAGGTGCAAGGCGATGGTCTCTGTGCATACCTGGGGGATGCCGGG  
CTCAGCTCCTCCCACTGCAGCACGCGGAGGAATTGGGTTTGCACCAAACC  
CGCGTTGCAAAAACCGAGGAAGAACTTCTGCATCAGCACCTGAGCGGCTC  
CCGGACCCGAACACGCGATGCAAGAGGAGGAACCCAAAGCAAAAGAGCTC  
CGCTTTCAGCTGTGCTCAGTAGCAACAGGAGGGCGGTGCGCTCCTCCAGC  
CCAGGTCCGACAGTGCCGCCTATGGGGCTGCGCGGACCGAAGCAAATCCC  
AGGCGGAGCTTCGGCTCCAAATTACATTTTTTTGCACCGTCTGACTCCTA  
ATGACCGCTAAAAATCCCAATTTTGGGGGCTATCCGTGCGCTGCTTGCAAC  
GACCTTCACCCCTGCGCGATGCAGCAGCAGGTTTGGGGGGCGGACGGTGG  
GAAAATATCCATTTTTCACCGGTTTTCTCAAAGGGAATACTGGGAAA  
GCAATCAGCCCAAAGGACCCTGAAATCGATGAATAAATCGGCAAATTATT  
TATGTTTTCGTGTTTTCCCTTCTGTGTCACTGCAGTGCCTTCTCCATGAAT  
TCACTTTTAACGGTGTTTTGTACAGGAAACACTTCTTCGACTCTCTCCA  
CCACTCCTATATATTCAACAGACCAATTCTTCTGGTGATTTTATGCAAA  
AACAAAAGAGTATATTGGTTAAAGAACCCAAACCACCTTCTTGTACTGA  
AGGGAATAGAAGAGCACAGACCGCCCGCTCCCTCCCTGCTGCCGCACA  
ACAGACGGTCCCCGAGGATGTGCAGACAACGCGACGCGCTCTGA

FIGURE 10

SUITE 61

WO 99/27132

PCT/FR98/02501

99/110

E6G2N15.txt

TAGNAACTAGNGGATCCCCCGGGCTGCAGCTATGGGGGAGTGGGTGCACT  
CCTTGGCCATGGCTTTGGGTCCCGTTACTCTGGAGGAATTTCCACAGCTG  
CCCCAGGAATCTTGTACATAAAAGTGCACAGATCGATCAGAGATGTCATG  
TTCCTGACAGAAGAAATCCTGTCTCTTCTGATGTTCTCTGTGAAGAGCAT  
TGCCACGAGGGAGCTACCAGCAGGGCAAGCAGAGAAATTGAAGAAAACGA  
AAGATGGGTGAGGTACGGGATTGGGCAGGTTTCACTTTCTTTAGCAATG  
AGACGTGTCAAGCTGGCAGCTTCCCTGGGAGCCTCTCTGGTGTGGATCTC  
CGGTGGCCCTAAACCTGGTTCAGGCACTGATCAAGGAGACATTACCCGTC  
TTGGTTCATCTCGGCTCACGG

FIGURE 10

SUITE 62



100/110  
F12FOR.txt

CGATGGTCCTCCAATGACCTCCATGGTCATCCAGTGCTCATCCCGCGGTA  
TGGCCATGGTAACCCCATGTTACCCCTGTGGTCTCACCCCAATGATGCCG  
TGTTTACCTTTTCGTTACCCCTATTCTCATCCCATATCCCCCTTTCTGTC  
CCTCTGCCCTTCATGATCCCCCTCATGGTTAACAGACGTTTCCCTCTGCCG  
ATCAGGTCATGTTACAGCACAAATTCCTCCAGGGTTCCTTTATAGTGACC  
TCACCATTACCCAATCATGTCCCCGGTGTCCCTGAAGGGGCCAGATTTT  
CTCAGTGGGACCCAGATGTCTTCAGTGGGGCGGGACCTGGCCATTCCCAA  
TGTCATCCAGGTGTCCATATGGCATGGGACACAGATGTGCACATGGGATG  
GGACCCAGGTGTCCCCACTGTTCATCCAGATGCCTCCATGGGTGGGAAAT  
GACCATCCTCGATGTCACCCAGATGCCACATGTGATGGGACGTGGCCAT  
CCTTCATGGCATCCCGATGTCCAGCTTGGGATGGGATCCCAATGTCACCC  
AATGCAATCGCAGTGTACCCAGATGTCCACAAGGGATGGCACCCAGATG  
TCCCCAGGTGCCACTCATCTGCCTCACCAACCCAGGACTTCCTCCCACTG  
CTCCCCACTGCTCCAGTTTGGCCCCATTTCTCCC

FIGURE 10

SUITE 63

101/110

G2M13.txt

GATCTTCAGTGATTTTCAGTGGTCTTTGGTGGTCTTCAGTGCTCTTCGTT  
GGTCTTTGACAAAGATGCAGAGGAGCACCGCTCCCAGACGGACCCCCCGG  
GGACCCCATTTGTGCCCATCCCCACTGGGACATGCAGCCATTGACCACAG  
CCCTCCGGCTGCGACCACTCACTGATTCTTATCCAAAGTCCACTCTTT  
GCACACTTACCTCCAATTTAGTGATAAGGATGTGGCGTGGGACCGTCCCA  
ATGGCCGCACACAAGTCCAGGTAGATGATATGGGATGACCATGAAGGGAT  
CACAGAGAGGAACACGGGGTGACCACGAGGAGCAACGAAGGAAACGCTGA  
GTGACCACGGGCAGAAAATGGTGTGACCATTAGGGGACAACGAGAGGGAA  
CAGAAGTAGTAAGGAGTGAGAATGGGGTGACAAAGAGGTGACCATGGCAT  
AACTTTGATAAGACCATTGGGTGACCGCAGGGTGATGGCCATACCATGGG  
GTGAGCACTGGATGACCATTGGAGGTCATTGGAGGACCATCGGGTGGGACG  
AGGGCCGTGGGGACACCCGTGGGGCGGTGGGACGGGGGACAGATGTCAGA  
AGGAGCCCCGCGGCGCAGAACTCTGCCTGGAGACGGGTGACGCCGCCCGG  
CGCCGCCCGCGCTCATTGGCCCTCCCCGCCCGGGCTCGCGGCTG  
GCGCGGGGTGCCGGTCCCCATCGTCCGGCGGCAGCAGCCATGGGGAGC  
GGGCGCTCCCGGCGCGGGGGCCGTGCTGGTGGCACTGCTGGCGCTGGG  
AGCCCCGCCCGCGCGCGGCACGCGGCCCTCGGGTGAGCTCGGAGCCGCGG  
CGCGGGGACGGCGCTGCGTCCCCCGGAGAAACCCCGGAGCCCTTCTG  
GCCGTGCGCAGCGCTCGGGGCTGCGGGGGGACGGAGGGCGGGGGGGGGCG  
GCGGAGCCGTGGGGGACGCGGGGCGGGGAGGGGGCGGGGGGTGTGGCG  
GGGGCGGCTGTGTGCCCTGACCGTGCCCTCTGCCCGCAGCGTTCTTCTT  
CTGCGGTGCCATATCCGAGTGCCACTACCTGAACGGCACCGAGCGGGTGA  
GGTATCTGCAAAGGTACATCTACAACCGGCAGCAGTTCACGCACTTCGAC  
AGCGACGTGGGGAAATTTGTGGCCGATTACCGCTGGGTGAGCCGCAAGC  
TGAATACTGGAACAGCAACGCCGAGCTTCTGGAGAACC GAATGAATGAAG  
TGGACAGGTTCTGCCGGCACAACTACGGGGGTGTGGAGTCTTTCACGGTG  
CAGAGGAGCGGTGAGTGCCGCGGGGCGCAGCGCGGACGGACGGGCAGGCG  
CCGCGCTCTGGCGGTGGTCCGACGCGCTCCCCCGTGCCCCGCACTGGA  
GCCCCAAGGTGAGGGTCTCGGCGCTGCAGTGGGGCTCCCTGCCCGAAACCG  
ACCGTCTGGCGTGCTACGTGACGGGCTTCTACCCGCCGGAGATCGAGGTG  
AAGTGGTTCTTGAACGGGCGGGAGGAGACGGAGCGCGTGGTGTCCACGGA  
CGTGATGCAGAACGGGGACTGGACGTACCAGGTGCTGGTGGTGTGGAGA  
CCGTCCCCGCGGCGCGGGGACAGCTACGTGTGCCGGGTGGAGCACGCCAGC  
CTGCGGCAGCCATCAGCCAGGCGTGGGGTAAGGCCCGGGGCCCTGCC  
CGCCGCGGGGGGAGCGGGAGCGCGGCCCGGGCGCTGAGCCGCCGCTTC  
GTCCCCGACAGCCCGCGGCGGACGCGGGCAGGAGCAAGCTGCTGACGGG  
CGTGGGGGGCTTCGTGCTGGGGCTCGTCTTCTGCGCTGGGGCTCTTCG  
TGTTCCTGCGCGGTGAGAAAGGTGAGCGCTGGGGAGGGGGGCTGCGCCGG  
GGGGGGTGGGAGCGGGGGG

FIGURE 10

SUIITE 64

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H421.txt

GCTCTAAGAACTAGTGGATCCCCCGGGCTGCAGGATTACCAAGTGTCCCAA  
CTGTTT"TTGCCAATCCAAGCCCTGCAAATGTACAAATATATTAAGTGGTT  
TCCTTAATAGACATCTTTATATCTCTCACCATCATTTAACGTTAACCTT  
ACTCTGCTTTCTTCTGTGAACAGAAAACAAATCGGAAGCCTCATATACA  
GGTGTTCAGAGGAAAATAGTAAGTGGTGATGAACTTGGAGAAGTTGTGA  
AGTGAAATATGGGAGCTACTGCCTCTGGAGGGAGGAAAATAAGGAACCAA  
TGAAAGATGCCAAGGTGAAGCAAATGAAGGACCAGCTGTTTGTGGCTAGA  
GCATACATATCCAGTATTGCTAAAATGCCTTCTCAAAGCAAGTTGACTCG  
GGATATGAAACAGAAATATCCAAGAGTTTGAGCGTATTCTTAGTGAAAGTT  
CTCAAGATGCTGACCTTCCACCACAGTAAGTTCTCTCCAGTTTGGGTTTA  
ATCATT"TTGTACTGAAAGTTTAGTTCTTACTGGAAAAGATTTTGTG  
GATTTCTAGTCACATGAATCTCTCCTAGTTTGCCTTCAGTTTGCCGGACA  
TCCCGT"TTTCTAGTGGTTTACTTGCTT

FIGURE 10

SUITE 65

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H4212.txt

TAACCATGAGTGATAAACTGCGGCCAACTTACTTCTGACAACGATCGGA  
GGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAAC  
TCGCCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACG  
AGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACCTA  
TTAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTG  
GATGGAGGCGGATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGG  
CTGGCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGC  
GGTATCATTGCAGCACTGGGGC

FIGURE 10

SUITE 66

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H424.txt

TCCCTAGTAACGGCCGCCAGTGTGCTGGAATTCGGCTTAGCGTGGTTCGCG  
GCCGAGGTACATACCCTGCCCCGAGTGATGTCTCCAAGGTTGATTTAAGC  
AACCAGCTCCTCCCTGCCACGGCTCCAGGCTCCACATGCCTGGGTTAAGG  
CTGGGTTTGTGTTTTTGGAGACAGTGTCTTAACATATGGAGCGCTGACTGTTT  
TGGAACCTCGCTCTGTAGACCAGTCTGGCCTTGAACCTCAGTGATCCCCCTG  
ACTCTGTCTCCAGAATGTGGATTCTCCCA

FIGURE 10

SUITE 67

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H4REV.txt

GGATTCTGACACCCCTCCTCCCCACCCCAAGGTGTTCCAGCGCCGCA  
TGGATGGGGGCACCGACTTCTGGAGGGGGTGGGAGGAGTACGTCCATGGC  
TTCGGGAACGTTTCTGGGGAGTTCTGGCTGGGTGAGGACCCCAAACTTG  
GGAAGATTGAGGTCTGGGGTGGGGGGGGGAACACCCAGGGCGGAGAGGG  
CTGATGGCTGCAGGACGTGGAGTGGGATCCCTGACGGGGGTGTGGGGTGG  
GGGGTGTGGGGCAGGGGCCCCAGGTGGGTGTGTAGGGTGGGGATGATGAC  
GATGGCTGTGGGATGTGGCGCAGGGAATGCGGCGCTGCACACACTGACAG  
CTTCCGGGCCCACGGAGCTGCGTGTGGACCTCTGGACGCCGTCAGACAGC  
GCCTTCGCCCCGCTATCGGGATTTCCCGTCAGTGGTCTTGAGGACAATTT  
CCGCTTACCTCGGGGCCCTACAGTGGCACAGCTGGTGTGTGTGGGGCAG  
TGGGAGCTCCTGGGGGATATTAGGGTTAACCTTGACCCATGAGGGGGGCT  
TTTGGGGATACCCAGATCAGGGGGGGGGGAATCCTGGGGAGAGTAGGGG  
ATGGTCCCTTTGCCACAGTGAGGGGGCCTTGCCCTGCAGAGGTCTTTAA  
GATCGTTGACCTGTTGGGATCTCTTGGGGATCTCCAGACTGCAGGGAGCC  
CCGGGGGTCTTGGGGGGCTCTGCCCCACAGGGTGGTCTCTGTGAGGGTG  
TGGGGGTACCTGGGGGGTCTGCGGCTCATCCTTGGGGCTCTGAATGCTAT  
GTGGGTGTCTTGAAGGCTCTCTTTAGGGGTCCCCATAACCTTGCTGTGG  
GTCCCACAGGGGATGCACTGTCTTACCATGCTGGGAGCCCTTCTCCACG  
CGGGACCACGACCCCCGAGGCCGCCCTCGGCCCTGCGCCGTGCGCTACAC  
CGGAGCCTGGTGCTACCGCAACTGCCACTACGCCAACCTCAATGGGCGCT  
ATGGGGTGCCCTACGACCACCAGGCATGGCTATGGGGGTGTAAAGGGGT  
CTGTGGGGATTGTAAAGGGGTCTATGGGGGTATAAAATCAACCCAATGGG  
ACAGGAGGGGGTCACCATGAGGCCATGGGGGTTTGTGGGGTAAATGTGG  
AGGGCTACCCCCCCCCAAGGTCCTTTTAGCCCCATGTCTCTCTGTATG  
AATATGGAGCCCTACAGGAGCTGTGGAAGCTGGAACACAAGCTGGAACAG  
GGAGGGGATACTTTGGGCCCCCTGTAAAGGCCTATATGTCTATAGGGT  
CAGGTAGGTTGTTTAAAGGCATGACCAAGTCCCCCTTCCTTTCTGCAGG  
GCATCAACTGGTACCCCTGGAAGGGCTTTGAGTACTCCATCCCCCTTACA  
GAGATGAAGCTGCGACCGCAGCGTGAAGTGAAGCACTAGAAAGGTCTGTGG  
GTCGAGTGGAGCCTTTATGGGGTCAATAAAGCTGCGAGTAGCCAGTGCT  
GACCCATGTATCCACACACTGGGCTCAGGAGCTATGGGGGTGGGCAGGG  
CGTGAGGCGCACGCGGAACGGGGCACAGCGCAGCACGGTGCCAGCAGTGA  
CCCCTAAGTGGGGCAGAGCCCCATCAGACGGTGGCTCCAGGCGGAATCGC  
TGTAGGATGTGCCCCAAAAACACAAAGAGCTCTGCCCCGAGCCAGCGCCTC  
CCCCACACAGAGCGTGCCCCACAACCAAAGGGCAGCAGCGCTCGCCATG  
GAGCCCCCGGCTGCAGGAACCGCTCTGTGGGGCAGAACAGAGATCAGAGT  
GGGTGTAGGGGGAGGAACCCAGCCTGGGGTTCAAAGCCCACATCTATGGG  
GTGGACCCACACATAACGGGCAGGAACCTCATCAGGACGGTCCCAAATCTT  
GGGGTCTGTGGTGCAGCAAAGAGGTTTGGGATAACGATGGATCCCGCAG  
GCACTGGGATTCCCGCAATGCTGGGAAGGGACAGAATGCTGATAGGATGG  
ACTGGGAGAGCCTACAGAGGCCAAGTGGGACATACTGGGACCTGCTGAGC  
TATCCTAGAGCTTACTGGGTGCTTGTAGTGTCTACTGGGACCGACCTAC  
TGGTAGGTCCATGCTGGTCTGTAGTGGTCCACACTATTACAGACTGGTCT  
ACAATGGTTTATTCTAGTGCAAAATACTGACACGAGTGGTGACGGTTC  
TGCTCGCAGACATGTGGCCCGCACTGGTTGGTACTGATCCCCACTGGTCT  
GTATGGCCCCATAACAGCCCGTACTGGTGTACTGGCTGTACCTGGAGTG  
GCGCCGGGCACAGTGGGGCAGCGGAGGGGCACGGGGGGTGCAGGCGGA  
GGGTCTCGGTGACAGTGGCAGGAGCAGTGGCAGTGGCCCCATATCCCT  
GGCTTTGGGGTCCCCCTGGGGCCAGCACCTGGCGCAGCTCTGCACGTAC  
CTGGTCTGCACCTGGGACAGGGGACACGTGTCAAAGCACGTCACCAAGT  
GCCACATCGGGTCACTTGTGGGGTGGCCCTCCCCTGCACGGGGACACAGG  
CAGCAGCGTGACACGGAAGTGACATGAGCGTGACATTTTGGCACTGGCCA  
CAGTGCAGGGGACACAGGGGCATTATGCACACAGGGTTATGGACATGGA  
TGTGACATGCATATGGGGAAGTGCACTGGAGCTATGGGAGGGGACAGCCA  
GGACATGGGTGGGGAGGCCGAATGGGACCTGGGGAGAGGAGGAGTGTGGG

FIGURE 10

SUIITE 68

TGTGACACAGATGTGATGTGGTGTACCTGGGGGTGGTGCAGCAGGAAGG  
CCACAGCCCATAGCAGAGCCACTGCCGTGCTTTTCGGTGCCACCGATGAAG  
AGATCCACGAGGGCCATGTGCAGGCGGTCCCCCCCCAGCGGCCCATAGG  
GACAGTGGGGTCCCCCCCCAGCAGTGCTCCAGCACTGTGTCCCTGGGGG  
GAGACGCACAGCCCTGTGGGGACACACGTGTTACCCCTGGGGCCCTGTC  
CCCCCCTGTACCTGTGTCCACGTTCCACCTGGTGCCATCGGATCT  
GGGACTCCACAAAGGCATCGCGGCGCTCCACCAGGCGCAGCAGCTCCCGC  
AGCCCTGCGTTGGGCAGCACCTGTGGGGCACAGGGACCCCCCAGTGCT  
CCACAGAGCACCCTGGACCCATAGGGACCCCATATTCCCTCCAGCCCC  
ATATATAACCCCCCCCCAGGGCGATATAGCCCATCCTTAGTATAGACCC  
TGCAGCCCCATATGGACCTATACCACCTCCTCTTATGACTATATCCCGCA  
GCCCCACGCCGATCCTATATGCCCTGTAGGGCCCTGTAGGGCTCACCCCTT  
AGTGAAGGCAGCACATCCAGTGCCCGCACACTGGCCCGGCCCCACACCTC  
CAGCAGTTCACCACACAGCGCGTGAAGGAGCGCACCTCCGCCTCGGGGG  
GCATCTGTGGGGCACAGGGCTTGGGGTCACCCCAGAGAGACTCCTGAGTC  
CCCCCAGAGACTCCTGAACCCAAAGAGGTACCGTGGTCAATTTGGATCCCT  
CTAGAGGTGACTGGGTTCCTAAAGGGACACCTCAACACTTGTGTCCCTT  
CAGGGGCACCTGGATATCTGGGACTCCAAGTGGCACCTGAGCATTGGGA  
CCCACCCTCCTTGGACACCTGGGTCACCCCAAGGACACCTGGGACCCCTT  
CAAGTGGCACGTGGACATCTGAGCCCCCTGTAGTGGCACTTGAGTCCCC  
TGCTCCCCCAGGTGACACCCAGACCCTGCAGCCCCCTCGATATCCCCACCA  
GGTCCCCGAAGGCAAGGCGGCAGATGGTGTGTCAGGTGTGGAACGTGAAC  
GCTTCAAAGAGGTCCACTGGGGCAGCCCCATAAGAGCTCAACTCCTGTGG  
GGTGAGAAATGGGGTCACTGAGCGGGTGCGGGTGCCCCACAAGGGGGGT  
GGGGTGAGTCAAGGGGACGGGCAGCACAGCCCTGGGGCTGATGGGGTCCA  
CCTGGGGTTGGAGGGCCCTGTGTGGGGTGTGTCACCTGGCACAGCGCCCA  
GCCCTGCAGCTCCAGGAGGGGCTCCAGGTGCCTCACAGCTCGCGCCAGTG  
CTCCCCGCTTGGCCCCCGCTGCCGTGCGCACTCTGGGGATGCATCCCC  
AGCGCCAGGTCTTCCCCCCCCCGGACACCAGGGACGCTGTGGGGTGACA  
CCCATATCACCTGGCACCCATGTGACCTCCGAGAACCCCTCAGACAGCT  
GTACGGATCCTTGGGGACACATCCAGAATCCCCCAGGCACCCACTGGGAT  
CGCTCCAGCACCCATGGGGACTGTTAGAGATCTCCTCCCCCCCCAAAAAT  
ACAACCAGACCCCTTCAAGATCATGGGGACCCCCCAGTACCCCTCCA  
GATACCCAACAGTGACCTATAGAGACCTCCTCCACCCAAAAGCCATGGG  
GACCCCTCAGGGCCCCCCCCCAGACACCAATTAGTACCCCCAGAACCT  
TCAGAAACCTACAAGGACCCACCAGAACCCCTCAGATACCCATAGAGAT  
CTTTACAGACCTCCTCCTGGGACCCTCCCCAGGAGCACAAATCCCAAAGA  
ACCCCTTGAAGATTACAGGGACCCCTCTGACTACCCCAAACCT  
CATGGGGACCTCCCAACCCCTACAGCCCCCCTATCCAGGTAACCTGTGG  
GGGCGTCCACGAAGTCCCCCAGCGCGGTGCCAGTGCCTCACGGATGGC  
TGCTGCAGAGCTCAGCACCACACCTCTGGGGGGGTGGGGGGGAGGGG  
AAAAATGAGTGAGTTGGAAGGAAGGGACCCATGGGGACCCAAAAACC  
AGGGAGAGGGAGAGGTGAGGGGTGCCAGAACGGAGTTGGGGGGGGGGG  
GGGAGGGATCCCAAATTATTTTTTGGGGGGGGGAGTAGAATGAGAGGAC  
AAATTTGAAGGGGAGCAGAAGGAATTGGGGGACAGTATGTGGGGGTTCC  
TCCATCCTCTCAATGGGTAATTCTGGGGAGCCTGTGAAGTTGAGGGTCT  
AAAGGGGAAGGCTCAAGGTCCCAAGGAGGAAGGGTTATGGGGAAAAGG  
GGGTAATGGTGGTCCCAAGGGGTATCAGGGGGATGGGGGGGGGGGGGGT  
CATGAAGGTGCCGCCCTACTCACCACACCCCCCAAGCGCAGGCATAAG  
GGGTCCCCGTAGGTCCGGGCAAGGATGTGGAGGTGCCGTGGCCCCCTGG  
GTGCAGGAGGTGCAGGGCCCCCCCCACGGTGCTCCCCCGCCTGGCTG  
ACCCCCCCAGATCAGAGCCAGGAGAAGTAGCAGCAGAAGTATCGTCACC  
GCCATTGTTCTGTGGGGTGGGGGGCCCCAGCTCTGCCCTATAACACCTT  
ATGAGGAGGAGGTACCCCAAAGCTCCACCCCCCACATCCAAACCCCTC  
CTACCAGAAGAGGGGCATTGGGTTCACTCCCCTAAAATTATTGTGTGCC

FEUILLE DE REMPLACEMENT (REGLE 26)

FIGURE 10

SUITE 69

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H4REV.txt

ACCCCCCTCTTCAAGTCATTATAAACTTTACAGGGGTGTCCTCATAAAAA  
TACAGGAGTGTGTCCCCCACAAAGTGCTCCCGAACCATCGGGTGCCCA  
TCCCACAAGAAAATCTCTCAAACCTCCCATTTGTGTGCCCCCAACCAACAA  
AGATTCTCTCAAACCTCCCCCCCCCGCCCTCTACCCATATATCTCTCCAAGC  
GCTCCCCACCCCTCCGCACACCACCTCCCCAAATCCTCCCCATTACCAT  
AATCCCCCCCCACCCAGCAGCAGAACCCCATCACCGCTCTGTGCGTCTGT  
GTGTGTGAGTAGGGGACGGGGTGTATTGAGGGGAGGGGGAGGGGGGA  
GAGCGCTCAGAACCCCTCCCCCTGCAGCCCCCGCAGGCGCCGTGCCAGCT  
GCAGGTCTTTGGGGTACAGTGTGACGCGGCGCGCATGCAGCGAGCACAGG  
TAGGCGTCTCTCCAGCAGGTGCACCAGGAATGCCTCCGCCGCCTGTGGGAC  
CCCGCGTGGGGTCCCCACAAAGCAGGGGGGGAGTCAATTCCCACCCCC  
AGGCCACCCCAAAATGCCAATCCTCCAAAATAATCCTGGAACAACCCC  
AAAAAAACCCCTACCCCCAACCCCTCCCCAAAACCATAACCTCAATAA  
CTCCACACCTCAAAAACCTCCAACCCCTCCAAAACAACCCCAACCCGA  
AACACCTCACCCCAAGACCCCTTCCCAAGCCCCAAAGAGACCCCAAGG  
CACAAGGGGTACCCCAAAATCCACTTCCCCCTTCCCCCAAAAAGCCCTT  
TTGGGCACTAGAGAGCTCCCCAGCACCCCAAGGGTCCCCACGGTAT  
GGGGTACCCTAAAACACCCCCCAACCCCAAAACCACGGGAACCTCCAAAAC  
AAAGCTACCCCTCCCCCCCCCCCCAAAAAATAAACCCATAGGGCCCC  
CCACCTCCTGTAGGGCCAATAGGGCCATAGCCTGCCACCTGTAGTCCACG  
CCCCGTGTGAAGAGCAAGCAGATCTCCCGCACCTGGGGGGGGACAGGGGG  
GCATGGGGACACTGGGGGGACATGGGGGGGGGGGGGGAGGGGGGGGGGG  
GGGAGGGGCATGAGGACATTGAGGAGAGGGAACACGAGGGTGGCACTGCA  
TCATGGGAGGTGACGAGGGGTGGGGGGGGCTCAAGGACATGGAGGGGGA  
CACTCA

FIGURE 10

SUIITE 70



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H6FOR.txt

TTGCTGCCTGCAGGTCGATCTAGTGGATCCGCCGCGACAGCGAACAGGCC  
AGCCAGCTGGTGCAGTATCTTTCCACTTTTTTCCGCAAAAACCTTAAAGCG  
GCCTTCGGAGTTTGTACTCTCGCCGACGAAATTGAACATGTGAATGCTT  
ATCTGCAAATTGAAAAGGCGCGCTTCCAGTCGCGGTTGCAGGTCAACATT  
GCTATTCCGCAAGAATTATCCAGCAGCAATTGCCCCGCGTTTACCCTGCA  
ACCC

FIGURE 10

SUITE 71

Conti205.txt

**SUITE 72**

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Conti205.txt

CATCCCACCCCTACAAGTTCAACCTTTACGGGGTGTGGGGGCAGACACGT  
CTGGGCCCCATCTCCACTGACACCATCACAGGTGAGGGCCCCCTGCCTGCT  
GCTGTGCTCTGGGCCCTTGTGCTTGGCACGTGGCAGGAGCTGTGCGATGGG  
CTGTGCTGGTGGCGGGGATCTGACTGGAAATGGAAACGTTCTGTGGCAAA  
GAGTGGGAATGTAGGAAGGGGGTGGGAGCATGCAGGGTTGGTGGAGCAGG  
GGGTAGTGATCAGTGGTGAGGATTTGGTTTCTTGGTCTGAAATATGGATG  
GAAGCTTTGTTGGGAGAGTGAATGACTTTTCAGTGAGGACAGGTGGATGC  
TTGGGTGAATGCTTGGTAAGTTGTTGAACGCCTGGATAGTTGGATGGGTG  
GACATGAACTTTGTATTACAGCTGCAGCTCCAGCACAGAAGGAACCGCCA  
TCCCAACCACGCCTGGGTGAGCTGACGGCCTCCCACGTGACCCCCGACTC  
CGTCCAGCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCACGG  
TGCAGTACAAGGATGCACAAGGCCAGCCACAGGTGGTGGCGTGGACGGT  
GGGTTGCGCACAGTGACCGTGCCCGGGCTGTGCGCGTCCCGCCGCTACAA  
GTTCAACCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTCCA  
CTGATGCTGTACAGGTGAGCATGCTGTTGTGCTGCATCCATGTCTTTTG  
GCTGACGGTTGTGTTGGCATATGGTAGGAACCTTTACAGGCCACTCCTGG  
TTACTGTGGTCTTAATAGAGAGGGAAGTTCTTTCCTGTTCTTGACGTGGG  
TAGCCTGGAGAGATGGGAGTATGGAAGATGAGAGGAAGAACGGAATAAGG  
AATGATTGATAATTATTGCAGAACGGATGGAAGGGAGGATGGATGGGCGG  
TGATGGTACATTTGGTGCTTATAGCAGAGCTGGACGGCTGGTTGTACGT  
TGGTTTGGTTGTTGAAGAGATGAAGAGTTGGATGGGCGTGTGCTTTTCACT  
GTGAATTCCTCCCCCTGTCTTGCAGCTCCGGCACAGAAGGAACCACTTC  
CCAGCCACTCTTGGGTGAGCTGACAGCGTCCCACGTGCGCCCCGACTCCG  
TCCAGCTGGAATGGAGCGTCCCCGAGGGCTCCTTTGACTCCTTCACGGTG  
CAGTACAAGGATGCACAAGGCCAGCCACAGGTGGTGGCGTGGACGGTGG  
GTTGCGCACAGTGACCGTGCCCCGGGCTGTGCGCGTCCCGCCGCTACAAGT  
TCAACCTGTATGGGGTGTGGGGGCGGAAGCGTCTGGGCCCCATGTCCACT  
GATGCTGTACAGGTGAGGGCAGGAATTGGCACCTGGTGGGCTCTGGGTT  
TGCAGCAGGTAGAAATGTAAACGTGGCCTGCGCTGGGGATCTTGTTCCTC  
CCTGGCAATGGGAACAGCTGTTGGGTGCCTTTTTTGGGAAGGATCCCTTA  
ATCGCAGCATGAAGTATGAATGGACCAATTGGGTGTGGGTGGAGTGATGG  
CTGTTGAGATGAGTTGGTGGCTGCTTGAAGTAATTGTCTGTTGGAATGGAT  
GGACAGATATGTGAAGGAGTGAAAGGATGGATAAAGTAATTTAGGAATCG  
GTGGATGAAGAATGGGTAGGTAGACCCTTGGTGAAGTGGTAGAATGGAAG  
GATTTATGAACAGATATGAGTTAATTCTTGCATCGAAGTAGGTGTAAGTG  
TCTATTAGCCTGTTGCACTGAACATGCAGTTGCATAGACAAATGAGTGGG  
GAGAAGTACGGAGTAAATCCCTGCATGAATGGTAGGACAGAAACCTGAAT  
GCCTGGATGCTGGCAGTGTGAAGAATGGCACTTGGGATAGATGGTTGAG  
TATGGGGTAGATTAAAAGATGGATGGAAAAGAGGAACAGAGAGAGGGTGA  
TTGGATGAATGGATGGATGGTTGGATGTGACTGATTGACAGGTACCAAGC  
TTTTTTCCTGCACTGTGCCTTCTGTGCTGCAGGACTATGGTCATAGCTGT  
TTCCTGTGTGAATTTGTTATCCGCTCACAAATCCACACAACATCGA

FIGURE 10

SUTTE 73

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/FR 98/02501

**A. CLASSIFICATION OF SUBJECT MATTER**  
IPC 6 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>GUILLEMOT F. ET AL.: "Physical linkage of a guanine nucleotide-binding protein-related gene to the chicken major histocompatibility complex" PROC. NATL. ACAD. SCI. USA, vol. 86, - June 1989 pages 4594-4598, XP002074404 See the whole document , esp. discussion -/--</p>	1

☒ Further documents are listed in the continuation of box C.

☐ Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

20 April 1999

Date of mailing of the international search report

03/05/1999

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Authorized officer

Müller, F

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/FR 98/02501

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>GUILLEMOT F. ET AL.,: "A molecular map of the chicken major histocompatibility complex: the class II beta genes are closely linked to the class I genes and the nucleolar organizer"</p> <p>THE EMBO JOURNAL, vol. 7, no. 9, - 1988 pages 2775-2785, XP002074405</p> <p>See the whole document , esp. figure 1 et page 2783, 2. colonne</p>	1
Y	<p>MILLER M. M. ET AL.,: "Regions of homology shared by Rftp-Y and major histocompatibility B complex genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 71-73, XP002074406</p> <p>see the whole document</p>	1-10
Y	<p>WAKENELL P. S. ET AL.,: "Association between the Rfp-Y haplotype and the incidence of Marek's disease in chicken"</p> <p>IMMUNOGENETICS, vol. 44, - 1996 pages 242-245, XP002074407</p> <p>see the whole document</p>	1-10
X	<p>BERNOT A. ET AL.,: "Linkage of a new member of the lectin supergene family to chicken MHC genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 221-229, XP002100550</p> <p>See the whole document , esp. p.221, col. 1; p.222 col.1</p>	7-10
X	<p>ZOOROB R. ET AL.,: "Chicken major histocompatibility complex class II B genes: analysis of interallelic and interlocus sequence variance"</p> <p>EUR. J. IMMUNOL., vol. 23, - 1993 pages 1139-1145, XP002074408</p> <p>see the whole document</p>	7-10
A	<p>VALLEJO R.L. ET AL.,: "Non-association between Rfp-Y major histocompatibility complex-like genes and susceptibility to Marek's disease virus induced tumours in 6.3x7.2 intercross chickens"</p> <p>ANIMAL GENETICS, vol. 28, - 5 October 1997 pages 331-337, XP002074409</p> <p>see the whole document</p>	

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# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/FR 98/02501

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>KAUFMAN J. ET AL.,: "Different features of the MHC class I heterodimer have evolved at different rates" J. IMMUNOLOGY, vol. 148, - 1 March 1992 pages 1532-1546, XP002074410 see the whole document -----</p>	

# RAPPORT DE RECHERCHE INTERNATIONALE

Deman internationale No  
PCT/FR 98/02501

A. CLASSEMENT DE L'OBJET DE LA DEMANDE  
CIB 6 C12Q1/68

Selon la classification internationale des brevets (CIB) ou à la fois selon la classification nationale et la CIB

B. DOMAINES SUR LESQUELS LA RECHERCHE A PORTE

Documentation minimale consultée (système de classification suivi des symboles de classement)  
CIB 6 C12Q

Documentation consultée autre que la documentation minimale dans la mesure où ces documents relèvent des domaines sur lesquels a porté la recherche

Base de données électronique consultée au cours de la recherche internationale (nom de la base de données, et si réalisable, termes de recherche utilisés)

C. DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	<p>GUILLEMOT F. ET AL.,: "Physical linkage of a guanine nucleotide-binding protein-related gene to the chicken major histocompatibility complex" PROC. NATL. ACAD. SCI. USA, vol. 86, - juin 1989 pages 4594-4598, XP002074404 Le document en entier, esp. discussion --- -/-</p>	1

☒ Voir la suite du cadre C pour la fin de la liste des documents

☐ Les documents de familles de brevets sont indiqués en annexe

° Catégories spéciales de documents cités:

- "A" document définissant l'état général de la technique, non considéré comme particulièrement pertinent
- "E" document antérieur, mais publié à la date de dépôt international ou après cette date
- "L" document pouvant jeter un doute sur une revendication de priorité ou cité pour déterminer la date de publication d'une autre citation ou pour une raison spéciale (telle qu'indiquée)
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Date à laquelle la recherche internationale a été effectivement achevée

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# **RAPPORT DE RECHERCHE INTERNATIONALE**

Demande internationale No

PCT/FR 98/02501

C.(suite) DOCUMENTS CONSIDERES COMME PERTINENTS

Catégorie	Identification des documents cités, avec, le cas échéant, l'indication des passages pertinents	no. des revendications visées
X	<p>GUILLEMOT F. ET AL.,: "A molecular map of the chicken major histocompatibility complex: the class II beta genes are closely linked to the class I genes and the nucleolar organizer"</p> <p>THE EMBO JOURNAL, vol. 7, no. 9, - 1988 pages 2775-2785, XP002074405</p> <p>le document en entier, esp. figure 1 et page 2783, 2. colonne</p>	1
Y	<p>MILLER M. M. ET AL.,: "Regions of homology shared by Rftp-Y and major histocompatibility B complex genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 71-73, XP002074406</p> <p>voir le document en entier</p>	1-10
Y	<p>WAKENELL P. S. ET AL.,: "Association between the Rfp-Y haplotype and the incidence of Marek's disease in chicken"</p> <p>IMMUNOGENETICS, vol. 44, - 1996 pages 242-245, XP002074407</p> <p>voir le document en entier</p>	1-10
X	<p>BERNOT A. ET AL.,: "Linkage of a new member of the lectin supergene family to chicken MHC genes"</p> <p>IMMUNOGENETICS, vol. 39, - 1994 pages 221-229, XP002100550</p> <p>voir le doc. en entier, esp. p.221, col. 1; p.222 col.1</p>	7-10
X	<p>ZOOROB R. ET AL.,: "Chicken major histocompatibility complex class II B genes: analysis of interallelic and interlocus sequence variance"</p> <p>EUR. J. IMMUNOL., vol. 23, - 1993 pages 1139-1145, XP002074408</p> <p>voir le document en entier</p>	7-10
A	<p>VALLEJO R.L. ET AL.,: "Non-association between Rfp-Y major histocompatibility complex-like genes and susceptibility to Marek's disease virus induced tumours in 6.3x7.2 intercross chickens"</p> <p>ANIMAL GENETICS, vol. 28, - 5 octobre 1997 pages 331-337, XP002074409</p> <p>voir le document en entier</p>	

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A	<p>KAUFMAN J. ET AL.,: "Different features of the MHC class I heterodimer have evolved at different rates"</p> <p>J. IMMUNOLOGY, vol. 148, - 1 mars 1992 pages 1532-1546, XP002074410</p> <p>voir le document en entier</p> <p>-----</p>	